

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:17:03 ; Search time 24.6053 Seconds  
(without alignments)  
1075.364 Million cell updates/sec

Title: US-08-949-904A-3  
Perfect score: 1487  
Sequence: 1 SARGLFLFGQDFSYKRSNC.....WQKGQREFKRISIRKLCQ 275  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1487	100.0	295	2 JE0174	frizzled protein-2
2	614	41.3	317	2 JE0175	frizzled protein-1
3	270.5	18.2	568	2 T25162	Frizzled-1 protein
4	269	18.1	647	2 JE0337	Frizzled-1 protein
5	264.5	17.8	537	2 JC7127	Frizzled protein 4
6	264.5	17.8	574	2 JE0339	Frizzled-7 protein
7	264.5	17.8	581	2 JC7086	FZD10 protein - hu
8	263.5	17.7	550	2 T37325	wingless protein r
9	259.5	17.5	641	2 A45054	probable intercell
10	256.5	17.2	565	2 JE0338	Frizzled-2 protein
11	241	16.2	694	2 S71786	wingless receptor
12	224.5	15.1	605	2 T31690	hypothetical prote
13	222	14.9	581	2 S03540	gene frizzled prot
14	216.5	14.6	666	2 JC7312	frizzled-3 protein
15	216.5	14.6	1113	2 JE0315	low-density lipopr
16	205.5	13.8	197	2 JC7735	frizzled-related p
17	201	13.5	706	2 JE0164	frizzled-6 protein
18	177.5	11.9	579	2 JC7629	membrane-type friz
19	149.5	10.1	1774	2 B56101	collagen alpha 1(X
20	133.5	9.0	526	2 T13484	frizzled protein h
21	119	8.0	581	2 B54665	netrin-2 precursor
22	96.5	6.5	793	2 JC5539	Smoothed protein
23	95.5	6.4	1282	2 JE0120	glycoprotein A - m
24	91	6.1	532	2 AE1964	Dnak-type molecula
25	91	6.1	1290	2 A55094	chromosomal protei
26	89.5	6.0	392	2 E81325	probable dihydroor
27	88.5	6.0	301	2 AE1989	hypothetical prote
28	88.5	6.0	606	2 A54665	netrin-1 precursor
29	88	5.9	3724	2 T18427	hypothetical prote

30	87.5	5.9	338	2	D97166	flagellar motor sw
31	87.5	5.9	366	2	D45558	epidermal growth f
32	87	5.9	761	2	D70447	tetrahydropteroylt
33	87	5.9	1014	2	T30545	major surface glyco
34	86.5	5.8	371	2	T34410	hypothetical prote
35	86.5	5.8	640	2	T19346	hypothetical prote
36	86.5	5.8	1342	2	A36223	kinase-related tra
37	86.5	5.8	2643	2	T29149	hypothetical prote
38	86	5.8	413	2	S52610	TYA protein - yeast
39	86	5.8	800	2	S13032	3',5'-cyclic-GMP p
40	86	5.8	856	2	S30762	3',5'-cyclic-GMP p
41	85.5	5.7	661	2	T42754	hypothetical prote
42	85	5.7	240	2	T33698	hypothetical prote
43	84.5	5.7	425	2	I59355	synaptotagmin IV -
44	84.5	5.7	727	2	T23585	hypothetical prote
45	84.5	5.7	1024	2	S71804	receptor-like serp

ALIGNMENTS

RESULT 1

JE0174  
frizzled protein-2 - human  
C:Species: Homo sapiens (man)  
C>Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JE0174  
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998  
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.  
A:Reference number: JE0174; MUID:98308108; PMID:9642118  
A:Accession: JE0174  
A:Molecule type: mRNA  
A:Residues: 1-295 <HUA>  
A:Cross-references: UNIPROT:Q9HAP5  
C:Genetics:  
A:Map position: 4q

Query Match	100.0%	Score 1487;	DB 2;	Length 295;
Best Local Similarity	100.0%	Pred. No. 1.5e-110;	Mismatches 0;	Indels 0;
Matches 275;	Conservative 0;			
QY	1	SARGLFLFGQDFSYKRSNC	KPIANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI	60
Db	21	SARGLFLFGQDFSYKRSNC	KPIANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI	80
QY	61	PLVMKQCHPDTKFLCSL	FAPVCLDDDETTPCHSLCVQVKDCAPVMSAFGPPWMDL	120
Db	81	PLVMKQCHPDTKFLCSL	FAPVCLDDDETTPCHSLCVQVKDCAPVMSAFGPPWMDL	140
QY	121	ECDRFPQNDLCIPLASSD	HLLPATEAPKVCACKKNDDNDIMETLCKNDFAKTKV	180
Db	141	ECDRFPQNDLCIPLASSD	HLLPATEAPKVCACKKNDDNDIMETLCKNDFAKTKV	200
QY	181	KEIYINRDTKIILETSKT	YIKLVNGVSRDLKSVLWKLDSLOCTCEMNDINAPYLVM	240
Db	201	KEIYINRDTKIILETSKT	YIKLVNGVSRDLKSVLWKLDSLOCTCEMNDINAPYLVM	260
QY	241	GQKGGLVITSVRWKQGR	EQREFKRISIRKLCQ	275
Db	261	GQKGGLVITSVRWKQGR	EQREFKRISIRKLCQ	295

RESULT 2

JE0175  
frizzled protein-1b - human  
C:Species: Homo sapiens (man)  
C>Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JE0175  
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998  
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.  
A:Reference number: JE0174; MUID:98308108; PMID:9642118



Best Local Similarity 40.0%; Pred. No. 2.7e-13;  
Matches 50; Conservative 20; Mismatches 48; Indels 7; Gaps 3;

QY 20 CKPTIPANLQCHGIEYQNMELPNLLGHETWKEVLEQAGAWIPVLMKQCHPDTKKFLCSLF 79  
Db 34 CQPII--BIPCKDIQYNTWRPNMLGHENREAAIQHEFAPLVEYCHGHLPFLCSLY 91  
QY 80 APVCLDDLETIQFCHSLCVQVDRDCAPVMSAFGFWPMDLECDRFPQDND--LCI--P 134  
Db 92 APMCTEQVSTPIACRVWCQFARLKSPINEQFNFKWPDSDLCRKLPNKNDPNVLCMEAP 151  
QY 135 LASSD 139  
Db 152 NNGSD 156

RESULT 8  
T37325  
wingless protein receptor Cfz2 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T37325  
R/Sato, A.; Koizumi, T.; Ui-Tei, K.; Miyata, Y.; Saigo, K.  
Development 126, 4421-4430, 1999  
A/Title: Drizzled-3, a new Drosophila Wnt receptor, acting as an attenuator of  
A/Reference number: Z21689; MUID:99429803; PMID:10498678  
A/Accession: T37325  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-550 <SAT>  
A/Cross-references: UNIPROT:Q9U8U6; EMBL:AB026113; NID:G5931529; PIDN:BAA84678.  
C/Genetics:  
A/Gene: Cfz2  
C/Superfamily: fruit fly frizzled protein  
C/Keywords: receptor; signal transduction; transmembrane protein

Query Match 17.7%; Score 263.5; DB 2; Length 550;  
Best Local Similarity 33.8%; Pred. No. 3.1e-13;  
Matches 54; Conservative 29; Mismatches 62; Indels 15; Gaps 4;

QY 7 LFCQPFYSKRSNCKDIPANLQICHGIEYQNMELPNLLGHETWKEVLEQAGAWIPVLMKQ 66  
Db 18 LFG-----KQCKEQI--TIPLCKGIGYNTMSPNSYGHKEQEEAGLEVHQFYPLVEVG 69  
QY 67 CHPDTKKFLCSLPAPVCLDDLETIQFCHSLCVQVDRDCAPVMSAFGFWPMDLECDRPP 156  
Db 70 CPOHLAFFLCTWPTICQENYDKPIPLCMELCVARSKSPINAKYGFWRPFTLSCEALP 129  
QY 127 QNDLCIPLASSDHLPLATEAPKVCEA---CKNKNDN 163  
Db 130 KMSD---QWSTGNICAAAPDTPKKQKHGHHKQNNQN 165

RESULT 9  
A45054  
probable intercellular signal transducer or transmitter Fz-1 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 02-Mar-2001  
C/Accession: A45054  
R/Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; H  
J. Biol. Chem. 267, 25202-25207, 1992  
A/Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely  
A/Reference number: A45054; MUID:93094228; PMID:1334084  
A/Accession: A45054  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-641 <CHA>  
A/Experimental source: UMR 106 osteosarcoma cell line  
A/Note: sequence extracted from NCBI backbone (NCBIP:120154)  
C/Superfamily: fruit fly frizzled protein

Query Match 17.5%; Score 259.5; DB 2; Length 641;  
Best Local Similarity 37.3%; Pred. No. 7.7e-13;







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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:54:34 ; Search time 107.105 Seconds  
(without alignments)  
1011.168 Million cell updates/sec

Title: US-08-949-904A-3

Perfect score: 1487

Sequence: 1 SARGLFLEQPDFSYKRSNC.....WKGQREFKRISIRKLCQ 275

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1487	100.0	275	8 US-08-949-904-3	Sequence 3, Appli
2	1487	100.0	295	8 US-08-949-904-2	Sequence 2, Appli
3	1487	100.0	295	14 US-10-177-293-142	Sequence 142, App
4	1487	100.0	295	15 US-10-295-027-1345	Sequence 1345, App
5	1487	100.0	295	16 US-10-783-528-107	Sequence 107, App
6	1487	100.0	295	17 US-10-847-972-78	Sequence 78, Appl
7	1487	100.0	295	17 US-10-432-256-2	Sequence 2, Appli
8	1483	99.7	295	9 US-09-978-295A-415	Sequence 415, App
9	1483	99.7	295	9 US-09-978-697-415	Sequence 415, App
10	1483	99.7	295	9 US-09-978-192A-415	Sequence 415, App
11	1483	99.7	295	9 US-09-999-832A-415	Sequence 415, App

12	1483	99.7	295	10 US-09-978-189-415	Sequence 415, App
13	1483	99.7	295	10 US-09-978-608A-415	Sequence 415, App
14	1483	99.7	295	10 US-09-978-585A-415	Sequence 415, App
15	1483	99.7	295	10 US-09-978-191A-415	Sequence 415, App
16	1483	99.7	295	10 US-09-978-403A-415	Sequence 415, App
17	1483	99.7	295	10 US-09-978-564A-415	Sequence 415, App
18	1483	99.7	295	10 US-09-999-833A-415	Sequence 415, App
19	1483	99.7	295	10 US-09-981-915A-415	Sequence 415, App
20	1483	99.7	295	10 US-09-978-824-415	Sequence 415, App
21	1483	99.7	295	10 US-09-918-585A-415	Sequence 415, App
22	1483	99.7	295	10 US-09-999-834A-415	Sequence 415, App
23	1483	99.7	295	10 US-09-978-423A-415	Sequence 415, App
24	1483	99.7	295	10 US-09-978-193A-415	Sequence 415, App
25	1483	99.7	295	10 US-09-999-830A-415	Sequence 415, App
26	1483	99.7	295	10 US-09-978-757A-415	Sequence 415, App
27	1483	99.7	295	10 US-09-978-187B-415	Sequence 415, App
28	1483	99.7	295	10 US-09-978-643A-415	Sequence 415, App
29	1483	99.7	295	10 US-09-978-375A-415	Sequence 415, App
30	1483	99.7	295	10 US-09-978-298A-415	Sequence 415, App
31	1483	99.7	295	10 US-09-978-188A-415	Sequence 415, App
32	1483	99.7	295	10 US-09-978-681A-415	Sequence 415, App
33	1483	99.7	295	10 US-09-978-194A-415	Sequence 415, App
34	1483	99.7	295	10 US-09-999-829A-415	Sequence 415, App
35	1483	99.7	295	10 US-09-978-299A-415	Sequence 415, App
36	1483	99.7	295	10 US-09-978-544A-415	Sequence 415, App
37	1483	99.7	295	10 US-09-978-665A-415	Sequence 415, App
38	1483	99.7	295	10 US-09-978-802A-415	Sequence 415, App
39	1483	99.7	295	11 US-09-999-831A-415	Sequence 415, App
40	1483	99.7	295	12 US-09-978-824-415	Sequence 415, App
41	1483	99.7	295	14 US-10-017-081A-415	Sequence 415, App
42	1483	99.7	295	14 US-10-167-749-415	Sequence 415, App
43	1483	99.7	295	14 US-10-013-921A-415	Sequence 415, App
44	1483	99.7	295	14 US-10-013-929A-415	Sequence 415, App
45	1483	99.7	295	14 US-10-016-177A-415	Sequence 415, App

#### ALIGNMENTS

RESULT 1  
US-08-949-904-3  
Sequence 3, Application US/08949904  
Publication No. US20030175855A1  
GENERAL INFORMATION:  
APPLICANT: Racis, Lisa  
APPLICANT: Lavallie, Edward  
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENETICS INSTITUTE, INC.  
STREET: 87 CAMBRIDGE PARK DRIVE  
CITY: CAMBRIDGE  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,904  
FILING DATE: October 15, 1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: LAZAR, STEVEN R.  
REGISTRATION NUMBER: 32,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8260  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 275 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-949-904-3

Query Match 100.0%; Score 1487; DB 8; Length 275;  
Best Local Similarity 100.0%; Pred. No. 9.5e-130;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60  
DB 1 SARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60  
QY 61 PLVMKQCHPDTKFKFLCSLFPAPVCLDDLDDETTQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120  
DB 61 PLVMKQCHPDTKFKFLCSLFPAPVCLDDLDDETTQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120  
QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180  
DB 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180  
QY 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
DB 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
QY 241 GOKGGELVITSVKRWKGOREFKRISRSIRKLOC 275  
DB 241 GOKGGELVITSVKRWKGOREFKRISRSIRKLOC 275

RESULT 2

US-08-949-904-2  
Sequence 2, Application US/08949904  
Publication No. US20030175855A1  
GENERAL INFORMATION:  
APPLICANT: Lavallie, Edward  
APPLICANT: Racie, Lisa  
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENETICS INSTITUTE, INC.  
STREET: 87 CAMBRIDGE PARK DRIVE  
CITY: CAMBRIDGE  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,904  
FILING DATE: October 15, 1997  
CLASSIFICATION: 336  
ATTORNEY/AGENT INFORMATION:  
NAME: LAZAR, STEVEN R.  
REGISTRATION NUMBER: 32,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8260  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-949-904-2

Query Match 100.0%; Score 1487; DB 8; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1e-129;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60  
DB 21 SARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKFKFLCSLFPAPVCLDDLDDETTQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120  
DB 81 PLVMKQCHPDTKFKFLCSLFPAPVCLDDLDDETTQPCHSVCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180  
DB 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 200  
QY 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
DB 201 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 260  
QY 241 GOKGGELVITSVKRWKGOREFKRISRSIRKLOC 275  
DB 261 GOKGGELVITSVKRWKGOREFKRISRSIRKLOC 295

RESULT 3

US-10-177-293-142  
Sequence 142, Application US/10177293  
Publication No. US20030124128A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Glatt, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Gannavaru, Manjula  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Mertens, Maureen  
APPLICANT: Myer, Vic  
APPLICANT: Wang, Youzhen  
APPLICANT: Xu, Yongyao  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Monahan, John  
APPLICANT: Meyers, Rachel E.  
APPLICANT: Bast Jr., Robert C.  
APPLICANT: Hortobagyi, Gabriel N.  
APPLICANT: Pusztai, Lajos  
APPLICANT: Meric, Funda  
APPLICANT: Sahin, Aysegul  
APPLICANT: Mills, Gordon B.  
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
FILE REFERENCE: MRI-038  
CURRENT APPLICATION NUMBER: US/10/177,293  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 60/299,887  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301,572  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/306,501  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/325,002  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/362,585  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
PRIOR FILING DATE: 2002-05-14  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 142  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-177-293-142

Query Match 100.0%; Score 1487; DB 14; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1e-129;



Publication No. US20050049195A1  
GENERAL INFORMATION:  
APPLICANT: ZOU, YIMIN  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION  
FILE REFERENCE: ARCD:395US  
CURRENT APPLICATION NUMBER: US/10/847,972  
CURRENT FILING DATE: 2004-05-17  
PRIOR APPLICATION NUMBER: 60/470,913  
PRIOR FILING DATE: 2003-05-15  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 78  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-847-972-78

Query Match 100.0%; Score 1487; DB 17; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1e-129;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI 60  
|||||  
DB 21 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI 80  
|||||

QY 61 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 120  
|||||  
DB 81 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 140  
|||||

QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDNDIMETLCKNDFALKIKV 180  
|||||  
DB 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDNDIMETLCKNDFALKIKV 200  
|||||

QY 181 KEITVINRDTKILLETKSTIYKLVNGVSRDLKKSVLWLKDSLOQTCSEMDNDINAPYLV 240  
|||||  
DB 201 KEITVINRDTKILLETKSTIYKLVNGVSRDLKKSVLWLKDSLOQTCSEMDNDINAPYLV 260  
|||||

QY 241 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 275  
|||||  
DB 261 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 295  
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RESULT 7  
US-10-432-256-2  
Sequence 2, Application US/10432256  
Publication No. US20050113291A1  
GENERAL INFORMATION:  
APPLICANT: Applied Research Systems ARS Holding N.V.  
TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma  
FILE REFERENCE: EP 469 Y  
CURRENT APPLICATION NUMBER: US/10/432,256  
CURRENT FILING DATE: 2003-12-12  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 2  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-432-256-2

Query Match 100.0%; Score 1487; DB 17; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1e-129;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI 60  
|||||  
DB 21 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI 80  
|||||

QY 61 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 120  
|||||  
DB 81 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 140  
|||||

QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDNDIMETLCKNDFALKIKV 180  
|||||

DB 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDFALKIKV 200  
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QY 181 KEITVINRDTKILLETKSTIYKLVNGVSRDLKKSVLWLKDSLOQTCSEMDNDINAPYLV 240  
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DB 201 KEITVINRDTKILLETKSTIYKLVNGVSRDLKKSVLWLKDSLOQTCSEMDNDINAPYLV 260  
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QY 241 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 275  
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DB 261 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 295  
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RESULT 8  
US-09-978-295A-415  
Sequence 415, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630FIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936  
 ; PRIOR FILING DATE: 1998-03-20  
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 ; PRIOR APPLICATION NUMBER: 60/082804  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082700  
 ; PRIOR FILING DATE: 1998-04-22  
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; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082796  
 ; PRIOR FILING DATE: 1998-04-23  
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 ; PRIOR APPLICATION NUMBER: 60/085582  
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 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1483; DB 9; Length 295;  
 Best Local Similarity 99.6%; Pred. No. 2.4e-129;  
 Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGPLFGQPDFSKYRNCCKPIPANLOI:CHGIEYQNMRLPNLLGHETMKVELEQAGAWI 60  
Db |||||  
21 SARGPLFGQPDFSKYRNCCKPIPNVQL:CHGIEYQNMRLPNLLGHETMKVELEQAGAWI 80  
QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQ:CHSLCVQVKDRCAPVMSAFGFPWPDML 120  
Db |||||  
81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQ:CHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPIASSDHLLPATEEAPKVC:CAKKNKDDNDIMETLCKNDFAFKIKV 180  
Db |||||  
141 ECDRFPQNDLCIPIASSDHLLPATEEAPKVC:CAKKNKDDNDIMETLCKNDFAFKIKV 200  
QY 181 KEITVINRDTKIILTKSKTIIYKLVGVSERD:LKKSVLWKDSLOQCTCEEMNDINAPYLVW 240  
Db |||||  
201 KEITVINRDTKIILTKSKTIIYKLVGVSERD:LKKSVLWKDSLOQCTCEEMNDINAPYLVW 260  
QY 241 GQKQGELVITSVKRWQKGQREFKRSIRKLCQ 275  
Db |||||  
261 GQKQGELVITSVKRWQKGQREFKRSIRKLCQ 295  
RESULT 9  
US-09-978-697-415  
; Sequence 415, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
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; PRIOR FILING DATE: 1997-11-13  
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; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
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; PRIOR APPLICATION NUMBER: 60/077649  
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; PRIOR APPLICATION NUMBER: 60/077791  
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; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
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; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21





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4	4	PRIOR FILING DATE: 1997-11-21	4	PRIOR APPLICATION NUMBER: 60/081952
5	5	PRIOR APPLICATION NUMBER: 60/077450	5	PRIOR FILING DATE: 1998-04-15
6	6	PRIOR FILING DATE: 1998-03-10	6	PRIOR APPLICATION NUMBER: 60/081838
7	7	PRIOR APPLICATION NUMBER: 60/077632	7	PRIOR FILING DATE: 1998-04-15
8	8	PRIOR FILING DATE: 1998-03-11	8	PRIOR APPLICATION NUMBER: 60/082568
9	9	PRIOR APPLICATION NUMBER: 60/077641	9	PRIOR FILING DATE: 1998-04-21
10	10	PRIOR FILING DATE: 1998-03-11	10	PRIOR APPLICATION NUMBER: 60/082569
11	11	PRIOR APPLICATION NUMBER: 60/077649	11	PRIOR FILING DATE: 1998-04-21
12	12	PRIOR FILING DATE: 1998-03-11	12	PRIOR APPLICATION NUMBER: 60/082704
13	13	PRIOR APPLICATION NUMBER: 60/077791	13	PRIOR FILING DATE: 1998-04-22
14	14	PRIOR FILING DATE: 1998-03-12	14	PRIOR APPLICATION NUMBER: 60/082804
15	15	PRIOR APPLICATION NUMBER: 60/078004	15	PRIOR FILING DATE: 1998-04-22
16	16	PRIOR FILING DATE: 1998-03-13	16	PRIOR APPLICATION NUMBER: 60/082700
17	17	PRIOR APPLICATION NUMBER: 60/078886	17	PRIOR FILING DATE: 1998-04-22
18	18	PRIOR FILING DATE: 1998-03-20	18	PRIOR APPLICATION NUMBER: 60/082797
19	19	PRIOR APPLICATION NUMBER: 60/078936	19	PRIOR FILING DATE: 1998-04-22
20	20	PRIOR FILING DATE: 1998-03-20	20	PRIOR APPLICATION NUMBER: 60/082796
21	21	PRIOR APPLICATION NUMBER: 60/078910	21	PRIOR FILING DATE: 1998-04-23
22	22	PRIOR FILING DATE: 1998-03-20	22	PRIOR APPLICATION NUMBER: 60/083336
23	23	PRIOR APPLICATION NUMBER: 60/078939	23	PRIOR FILING DATE: 1998-04-27
24	24	PRIOR FILING DATE: 1998-03-20	24	PRIOR APPLICATION NUMBER: 60/083322
25	25	PRIOR APPLICATION NUMBER: 60/079294	25	PRIOR FILING DATE: 1998-04-28
26	26	PRIOR FILING DATE: 1998-03-25	26	PRIOR APPLICATION NUMBER: 60/083392
27	27	PRIOR APPLICATION NUMBER: 60/079656	27	PRIOR FILING DATE: 1998-04-29
28	28	PRIOR FILING DATE: 1998-03-26	28	PRIOR APPLICATION NUMBER: 60/083495
29	29	PRIOR APPLICATION NUMBER: 60/079664	29	PRIOR FILING DATE: 1998-04-29
30	30	PRIOR FILING DATE: 1998-03-27	30	PRIOR APPLICATION NUMBER: 60/083496
31	31	PRIOR APPLICATION NUMBER: 60/079689	31	PRIOR FILING DATE: 1998-04-29
32	32	PRIOR FILING DATE: 1998-03-27	32	PRIOR APPLICATION NUMBER: 60/083499
33	33	PRIOR APPLICATION NUMBER: 60/079663	33	PRIOR FILING DATE: 1998-04-29
34	34	PRIOR FILING DATE: 1998-03-27	34	PRIOR APPLICATION NUMBER: 60/083545
35	35	PRIOR APPLICATION NUMBER: 60/079728	35	PRIOR FILING DATE: 1998-04-29
36	36	PRIOR FILING DATE: 1998-03-27	36	PRIOR APPLICATION NUMBER: 60/083554
37	37	PRIOR APPLICATION NUMBER: 60/079786	37	PRIOR FILING DATE: 1998-04-29
38	38	PRIOR FILING DATE: 1998-03-27	38	PRIOR APPLICATION NUMBER: 60/083558
39	39	PRIOR APPLICATION NUMBER: 60/079920	39	PRIOR FILING DATE: 1998-04-29
40	40	PRIOR FILING DATE: 1998-03-30	40	PRIOR APPLICATION NUMBER: 60/083559
41	41	PRIOR APPLICATION NUMBER: 60/079923	41	PRIOR FILING DATE: 1998-04-29
42	42	PRIOR FILING DATE: 1998-03-30	42	PRIOR APPLICATION NUMBER: 60/083500
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45	45	PRIOR APPLICATION NUMBER: 60/080107	45	PRIOR FILING DATE: 1998-04-30
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54	54	PRIOR FILING DATE: 1998-04-01	54	PRIOR APPLICATION NUMBER: 60/084639
55	55	PRIOR APPLICATION NUMBER: 60/080333	55	PRIOR FILING DATE: 1998-05-07
56	56	PRIOR FILING DATE: 1998-04-01	56	PRIOR APPLICATION NUMBER: 60/084640
57	57	PRIOR APPLICATION NUMBER: 60/080334	57	PRIOR FILING DATE: 1998-05-07
58	58	PRIOR FILING DATE: 1998-04-01	58	PRIOR APPLICATION NUMBER: 60/084598
59	59	PRIOR APPLICATION NUMBER: 60/081070	59	PRIOR FILING DATE: 1998-05-07
60	60	PRIOR FILING DATE: 1998-04-08	60	PRIOR APPLICATION NUMBER: 60/084600
61	61	PRIOR APPLICATION NUMBER: 60/081049	61	PRIOR FILING DATE: 1998-05-07
62	62	PRIOR FILING DATE: 1998-04-0		

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; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.7%; Score 1483; DB 9; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGLFLFCQDPFSYKRSNCKIPANLQLCHGIEYQNMRLPNLLGHETMKVLEQAGAWI 60
Db 21 SARGLFLFCQDPFSYKRSNCKIPVNLQLCHGIEYQNMRLPNLLGHETMKVLEQAGAWI 80

QY 61 PLVMKQCHPDTKFKLCSLPAPVCLDDLDDETIOPCHSLCVQVKDRCAPVMSAFGFPWDM 120
Db 81 PLVMKQCHPDTKFKLCSLPAPVCLDDLDDETIOPCHSLCVQVKDRCAPVMSAFGFPWDM 140

QY 121 ECDRFPQNDLCIPLASSDHLHPATEEAPKVCCEAKGNKNDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLCIPLASSDHLHPATEEAPKVCCEAKGNKNDNDIMETLCKNDFALKIKV 200

QY 181 KEITYNRDTKILLETKSTIYKLVNGVSERDLKKSVLWLKDSLQTCCEMNDINAPYLV 240
Db 201 KEITYNRDTKILLETKSTIYKLVNGVSERDLKKSVLWLKDSLQTCCEMNDINAPYLV 260

QY 241 GOKQGGELVITSVKRWQKQREFKRSIRKLQC 275
Db 261 GOKQGGELVITSVKRWQKQREFKRSIRKLQC 295

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; Sequence 415, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697  
; PRIOR APPLICATION NUMBER: 60/085697  
Query Match 99.7%; Score 1483; DB 9; Length 295;  
Best Local Similarity 99.6%; Pred. No. 2.4e-129;  
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
Db 21 SARGLFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
Qy 61 PLVMKQCHPDTKFLCSLFPAPVCLDDLDDETITQCHSLCVQVKDRCAPVNSAFGFPWPDML 120  
Db 81 PLVMKQCHPDTKFLCSLFPAPVCLDDLDDETITQCHSLCVQVKDRCAPVNSAFGFPWPDML 140  
Qy 121 ECDRFPQDNDLCIPLASSDHLLPATEAPKVEACKNKNDNDIMETLCKNDFALKIKV 180  
Db 141 ECDRFPQDNDLCIPLASSDHLLPATEAPKVEACKNKNDNDIMETLCKNDFALKIKV 200  
Qy 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCEEMNDINAPYLVM 240  
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCEEMNDINAPYLVM 260  
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; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavina, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1483; DB 10; Length 295;

Best Local Similarity 99.6%; Pred. No. 2.4e-129;

Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKVELEQAGAWI 60  
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Qy 21 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKVELEQAGAWI 80  
Db |||||  
Qy 61 PLVMKQCHPDTKKFLCSLFAVPCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 120  
Db |||||  
Qy 81 PLVMKQCHPDTKKFLCSLFAVPCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 140  
Db |||||  
Qy 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 180  
Db |||||  
Qy 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 200  
Db |||||  
Qy 181 KEITYINRDTKIILETKSTIYKLVGVSERDLKKSVLWKDSLOQCTCEMNDINAPYLVM 240  
Db |||||  
Qy 201 KEITYINRDTKIILETKSTIYKLVGVSERDLKKSVLWKDSLOQCTCEMNDINAPYLVM 260  
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## RESULT 13

US-09-978-608A-415

; Sequence 415, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kllavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C22  
; CURRENT APPLICATION NUMBER: US/09/978,608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 415  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-608A-415

Query Match 99.7%; Score 1483; DB 10; Length 295;

Best Local Similarity 99.6%; Pred. No. 2.4e-129;

Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 180  
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## RESULT 14

US-09-978-585A-415

; Sequence 415, Application US/09978585A

; Publication No. US20030049633A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-415

Query Match          99.7%; Score 1483; DB 10; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSKRSNCKPIPANLQLCHGIEYQNMRLPNLLGHETMKVELEQAGAWI 60
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; Publication No. US20030050239A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1479	99.5	296	4	US-09-148-545-237 Sequence 237, App
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4	1033	69.5	212	4	US-08-937-067-4 Sequence 4, Appli
5	614	41.3	305	4	US-09-949-016-7706 Sequence 7706, Ap
6	614	41.3	317	4	US-08-937-067-6 Sequence 6, Appli
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9	602	40.5	338	4	US-09-546-043-4 Sequence 4, Appli
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17	479	31.9	267	4	US-09-546-043-7 Sequence 7, Appli
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23	275	18.5	685	4	US-08-937-067-14 Sequence 14, Appli
24	264.5	17.8	572	4	US-08-937-067-13 Sequence 13, Appli
25	264	17.8	537	4	US-08-937-067-11 Sequence 11, Appli
26	260.5	17.5	114	4	US-09-087-031E-15 Sequence 15, Appli
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36	238	16.0	229	4	US-09-546-043-8 Sequence 8, Appli
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42	227	15.3	111	4	US-09-087-031E-9 Sequence 9, Appli
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44	219	14.7	111	4	US-09-087-031E-16 Sequence 16, Appli
45	218.5	14.7	666	4	US-08-937-067-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-09-148-545-179  
; Sequence 179, Application US/09148545  
; Patent No. 6590075  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: PZ001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: PCT/US98/04482  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,161  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
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; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
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; EARLIER APPLICATION NUMBER: 60/047,583  
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; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
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; EARLIER FILING DATE: 1997-05-23



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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 295

Query Match          99.5%; Score 1479; DB 4; Length 295;
Best Local Similarity 99.3%; Pred. No. 2.8e-154;
Matches 273; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 237, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
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; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-2

Query Match          99.1%; Score 1474; DB 4; Length 295;
Best Local Similarity 98.9%; Pred. No. 9.8e-154;
Matches 272; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGLFLEFGQDPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGLFLEFGQDPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
QY 61 PLVMKQCHPDTKFKLCSLFAPVCLDDLDDETTQPCHSKLCVQVKDRCAPVMSAFGFPWDM 120
Db 81 PLVMKQCHPDTKFKLCSLFAPVCLDDLDDETTQPCHSKLCVQVKDRCAPVMSAFGFPWDM 140
QY 121 ECDRFPQNDLICIPLASSDHLLPATEEAPKVCCEACKNKDDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLICIPLASSDHLLPATEEAPKVCCEACKNKDDNDIMETLCKNDFALKIKV 200
QY 181 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEBMNDINAPYLVM 240
Db 201 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEBMNDINAPYLVM 260
QY 241 GOKQGGELVITSVKRWQKQREPKRSIRSKLQ 275
Db 261 GOKQGGELVITSVKRWQKQREPKRSIRSKLQ 295

RESULT 4
US-08-937-067-4
; Sequence 4, Application US/08937067.
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Unanaky, Samuil
; APPLICANT: Meikonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-4

Query Match          69.5%; Score 1033; DB 4; Length 212;
Best Local Similarity 99.5%; Pred. No. 2.2e-105;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGLFLEFGQDPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGLFLEFGQDPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
QY 61 PLVMKQCHPDTKFKLCSLFAPVCLDDLDDETTQPCHSKLCVQVKDRCAPVMSAFGFPWDM 120
Db 81 PLVMKQCHPDTKFKLCSLFAPVCLDDLDDETTQPCHSKLCVQVKDRCAPVMSAFGFPWDM 140
QY 121 ECDRFPQNDLICIPLASSDHLLPATEEAPKVCCEACKNKDDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLICIPLASSDHLLPATEEAPKVCCEACKNKDDNDIMETLCKNDFALKIKV 200
QY 181 KEITYINR 188
Db 201 KEITYINR 208

RESULT 5
US-09-949-016-7706
; Sequence 7706, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7706
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7706

Query Match          41.3%; Score 614; DB 4; Length 305;
Best Local Similarity 46.7%; Pred. No. 5.1e-59;
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;

QY 14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72
Db 34 SYSKPPQCLDIPADLPCHTGVYKRMRLPNLLEHSAEVAQVQASSMLPLAKRCHSDTQ 93
QY 73 KFLCSLFAPVCLDDLDDETTQPCHSKLCVQVKDRCAPVMSAFGFPWDMLECDRFPQNDL 132
Db 94 VFLCSLFAPVC---LDRPIYPCRSCLCEAVRAGCAPLMEAYGFPWPEMLHCHKFLDNDLC 150
QY 133 IPLASSDHLLPATEEAP---KVCEACKNKDDNDIMETLCKNDFALKIKVKEITYINR 189
Db 151 IAVQFGH--LPAT--APPVTKICACEWEHSADG-LMEQMCSSDFVVKMRKEIKIENG 205
QY 190 TKIILETKSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEEMNDINAPYLVMGKQGGELV 249
Db 206 RKLIGAQKKKLLKPGPLKRDTRKLVLMKNGAGCCPCQLDSLAGSLVMGRKVDGQLL 265
QY 250 ITSVKRWQKQREPK 264
Db 266 LMAVYRWDDKKNKEMK 280

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RESULT 6  
US-08-937-067-6  
; Sequence 6, Application US/08937067  
; Patent No. 6433155  
; GENERAL INFORMATION:  
; APPLICANT: Umansky, Samuil  
; APPLICANT: Melkonyan, Hovsep  
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING  
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/937,067  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20018.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 317 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-937-067-6

Query Match 41.3%; Score 614; DB 4; Length 317;  
Best Local Similarity 46.7%; Pred. No. 5.4e-59;  
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;  
QY 14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72  
Db 46 SYSKPPQCLDIPADLPCHTVGYKRMRLPNLLEHESLAEVKKQASSWLPPLAKRCHSDTQ 105  
QY 73 KFLCSLPAPVCLDDLETIQPCHSLCVQVKRCAPVMSAFGPPWPDMLECDRFPQDNDLC 132  
Db 106 VFLCSLPAPVC--LDRPIYPCSLCEAVRACAPLMEAYGFPWPEMLHCHKFPLDNDLC 162  
QY 133 IPLASDHLLPATEAP---KVCEACKNNKDDNDIMETLCKNDPALKIKVKEITYINRD 189  
Db 163 IAVQFGH--LPAT--APPVTKICAQCEMEHSADG-LMEQMCSSDFVVKMKRIKEIKIENG 217  
QY 190 TKIILETSKTIYKLVNGVSRDLKSVLWKDSLQCTCEEMNDINAPVLVMGOKOGGELV 249  
Db 218 RKLIGAQKKKKLPGPLKRDTRKLVLMKNGAGCPCPQLDSLAGSFLVMGRKVDGQL 277  
QY 250 ITSVRKRWQKQREFK 264  
Db 278 LMAVYRWKKNKEMK 292

RESULT 7  
US-09-949-016-6300  
; Sequence 6300, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6300  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6300

Query Match 41.3%; Score 614; DB 4; Length 317;  
Best Local Similarity 46.7%; Pred. No. 5.4e-59;  
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;  
QY 14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72  
Db 46 SYSKPPQCLDIPADLPCHTVGYKRMRLPNLLEHESLAEVKKQASSWLPPLAKRCHSDTQ 105  
QY 73 KFLCSLPAPVCLDDLETIQPCHSLCVQVKRCAPVMSAFGPPWPDMLECDRFPQDNDLC 132  
Db 106 VFLCSLPAPVC--LDRPIYPCSLCEAVRACAPLMEAYGFPWPEMLHCHKFPLDNDLC 162  
QY 133 IPLASDHLLPATEAP---KVCEACKNNKDDNDIMETLCKNDPALKIKVKEITYINRD 189  
Db 163 IAVQFGH--LPAT--APPVTKICAQCEMEHSADG-LMEQMCSSDFVVKMKRIKEIKIENG 217  
QY 190 TKIILETSKTIYKLVNGVSRDLKSVLWKDSLQCTCEEMNDINAPVLVMGOKOGGELV 249  
Db 218 RKLIGAQKKKKLPGPLKRDTRKLVLMKNGAGCPCPQLDSLAGSFLVMGRKVDGQL 277  
QY 250 ITSVRKRWQKQREFK 264  
Db 278 LMAVYRWKKNKEMK 292

RESULT 8  
US-09-546-043-3  
; Sequence 3, Application US/09546043  
; Patent No. 6600018  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffery et al.,  
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 53990  
; CURRENT APPLICATION NUMBER: US/09/546,043  
; CURRENT FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-546-043-3

Query Match 40.5%; Score 602; DB 4; Length 313;  
Best Local Similarity 41.0%; Pred. No. 1.1e-57;  
Matches 118; Conservative 56; Mismatches 94; Indels 20; Gaps 6;  
QY 1 SARGL-----PLFCQPD-----FSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHE 47  
Db 25 SGRGLGSEYDVVSFQSDIGPYQSGRFYTKPPQCVDPADLRLCHNVGKVMKVLNLLSHE 84

QY 48 TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 107  
Db 85 TMAEVKQQAASSWVPLLNKNCHAGTQVFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 141  
QY 108 VMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLHPATEAPKVCCEACKNKNDDNDIME 167  
Db 142 VMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIE 199  
QY 168 TLCKNDPALKIKVEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTC 227  
Db 200 HLCASEFALRMKIKEVKKENGDKKIV--PKKKKPLKLGPIKKDLKLVLYLKNKGADCP 257  
QY 228 EBMNDINAPYLVMOQKQSGELVITSVKRWKQKOREFKRISRSIRKLQC 275  
Db 258 HQLDNLSSHFLINGRKVKSQYLLTAIHKWDKKNKEFKNFKMKNHEC 305

## RESULT 9

US-09-546-043-4  
; Sequence 4, Application US/09546043  
; Patent No. 6600018  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffery et al.,  
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 53990  
; CURRENT APPLICATION NUMBER: US/09/546,043  
; CURRENT FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-546-043-4

Query Match 40.5%; Score 602; DB 4; Length 338;  
Best Local Similarity 41.0%; Pred. No. 1.2e-57;  
Matches 118; Conservative 56; Mismatches 94; Indels 20; Gaps 6;

QY 1 SARGL-----FLFGQPD-----PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHE 47  
Db 25 SGRGLSEYDYVSFOSDIGYSGRYTKPPQCVDPADLRLCHNVGYKQWVLPNLLHE 84  
QY 48 TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 107  
Db 85 TMAEVKQQAASSWVPLLNKNCHAGTQVFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 141  
QY 108 VMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLHPATEAPKVCCEACKNKNDDNDIME 167  
Db 142 VMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIE 199  
QY 168 TLCKNDPALKIKVEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTC 227  
Db 200 HLCASEFALRMKIKEVKKENGDKKIV--PKKKKPLKLGPIKKDLKLVLYLKNKGADCP 257  
QY 228 EBMNDINAPYLVMOQKQSGELVITSVKRWKQKOREFKRISRSIRKLQC 275  
Db 258 HQLDNLSSHFLINGRKVKSQYLLTAIHKWDKKNKEFKNFKMKNHEC 305

## RESULT 10

US-09-514-885-1  
; Sequence 1, Application US/09514885  
; Patent No. 6656461  
; GENERAL INFORMATION:  
; APPLICANT: D'Armiento, Jeanine  
; APPLICANT: Imai, Kazuishi  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE  
; FILE OF INVENTION: PULMONARY DISEASE  
; FILE REFERENCE: 58483.app  
; CURRENT APPLICATION NUMBER: US/09/514,885  
; CURRENT FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Human  
US-09-514-885-1

Query Match 40.4%; Score 600.5; DB 4; Length 313;  
Best Local Similarity 42.6%; Pred. No. 1.6e-57;  
Matches 112; Conservative 54; Mismatches 90; Indels 7; Gaps 4;

QY 13 PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHEITMKEVLEQAGAWIPLVMKQCHPDTK 72  
Db 50 FYTKPPQCVDPADLRLCHNVGYKQWVLPNLLHEITMAEVKQQAASSWVPLLNKNCHAGTQ 109  
QY 73 KFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWPMLECDRFPQDNDLC 132  
Db 110 VFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWPMLECDRFP-EGDVC 165  
QY 133 IPLASSDHLHPATEAPKVCCEACKNKNDDNDIMETLCKNDPALKIKVEITYINRDTKI 192  
Db 166 IAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIEHLCASEFALRMKIKEVKKENGDKKI 224  
QY 193 ILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTCEEMNDINAPYLVMOQKQSGELVITS 252  
Db 225 V--PKKKKPLKLGPIKKDLKLVLYLKNKGADCPCHQDNLSSHFLINGRKVKSQYLLTA 282  
QY 253 VKRWKQKOREFKRISRSIRKLQC 275  
Db 283 IHKWDKKNKEFKNFKMKNHEC 305

## RESULT 11

US-09-949-016-6299  
; Sequence 6299, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6299  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6299

Query Match 40.4%; Score 600.5; DB 4; Length 313;  
Best Local Similarity 42.6%; Pred. No. 1.6e-57;  
Matches 112; Conservative 54; Mismatches 90; Indels 7; Gaps 4;

QY 13 PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHEITMKEVLEQAGAWIPLVMKQCHPDTK 72  
Db 50 FYTKPPQCVDPADLRLCHNVGYKQWVLPNLLHEITMAEVKQQAASSWVPLLNKNCHAGTQ 109  
QY 73 KFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWPMLECDRFPQDNDLC 132  
Db 110 VFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWPMLECDRFP-EGDVC 165  
QY 133 IPLASSDHLHPATEAPKVCCEACKNKNDDNDIMETLCKNDPALKIKVEITYINRDTKI 192  
Db 166 IAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIEHLCASEFALRMKIKEVKKENGDKKI 224





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Db 45 YGSGRFYTKPPGCVDPADLRICHNVGYKQWLPNLLHETWAEVKGASSWVPLLNKNC 104
Qy 68 HPDTKKFLCSLPAPVCLDLDLDTIQCHSLCVQVKDRCAPVMSAFGFPWPDMLCDRFPQ 127
Db 105 HAGTGVFLCSLPAPVC---LDRPIYFCRWLCEAVRDSCEPVMGFFGYWPEMLKCDKFP- 160
Qy 128 DNDLCIPLASSDHLPLATEAPK-----VCEACKNKNDNDNDIMETLCKNDFAIKIKVKE 182
Db 161 EGDVCIAMTP-----PNATEASKPGGTTVCPDCDNLKSE-AIIHLCASEFALRMKIKE 214
Qy 183 ITYINRDTKIILTKSKTIYKLVGSEDLKKSVLWLDLSLOCTCEEMNDINAPYLVMQ 242
Db 215 VKKNGDKKIV--PKKKPLKLGPIKKDKLKKLVLYLKNAGDCPCCHGLDNLSHHFLIMGR 272
Qy 243 KGGELVITSVKRWQKGQREFKRISIRKLOC 275
Db 273 KVKGYLLTAIHKWDKKNKEFNFMKMKKNHEC 305

RESULT 15
US-09-087-031E-3
; Sequence 3, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-3

Query Match 39.2%; Score 583.5; DB 4; Length 314;
Best Local Similarity 42.5%; Pred. No. 1.2e-55;
Matches 116; Conservative 48; Mismatches 92; Indels 17; Gaps 6;

Qy 8 FQOPDFSFKRSCKPIPANLQICHGIEYQNMELPNLLGHETMKEVLEQAGAWIPLVMKQC 67
Db 46 YGSGRFYTKPPGCVDPADLRICHNVGYKQWLPNLLHETWAEVKGASSWVPLLNKNC 105
Qy 68 HPDTKKFLCSLPAPVCLDLDLDTIQCHSLCVQVKDRCAPVMSAFGFPWPDMLCDRFPQ 127
Db 106 HAGTGVFLCSLPAPVC---LDRPIYFCRWLCEAVRDSCEPVMGFFGYWPEMLKCDKFP- 161
Qy 128 DNDLCIPLASSDHLPLATEAPK-----VCEACKNKNDNDNDIMETLCKNDFAIKIKVKE 182
Db 162 EGDVCIAMTP-----PNATEASKPGGTTVCPDCDNLKSE-AIIHLCASEFALRMKIKE 215
Qy 183 ITYINRDTKIILTKSKTIYKLVGSEDLKKSVLWLDLSLOCTCEEMNDINAPYLVMQ 242
Db 216 VKKNGDKKIV--PKKKPLKLGPIKKDKLKKLVLYLKNAGDCPCCHGLDNLSHHFLIMGR 273
Qy 243 KGGELVITSVKRWQKGQREFKRISIRKLOC 275
Db 274 KVKGYLLTAIHKWDKKNKEFNFMKMKKNHEC 306
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OM protein - protein search, using sw model

Run on: September 1, 2005, 09:41:17 ; Search time 112.412 Seconds  
(without alignments)  
946.152 Million cell updates/sec

Title: US-08-949-904A-3  
Perfect score: 1487  
Sequence: 1 SARGFLFGQPDFSYKRSNC.....WKGQREFKRISIRKILQC 275

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980a:\*

2: Geneseq1990a:\*

3: Geneseq2000a:\*

4: Geneseq2001a:\*

5: Geneseq2002a:\*

6: Geneseq2003a:\*

7: Geneseq2003bs:\*

8: Geneseq2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1487	100.0	275	7	Adf77694 Human mat
2	1487	100.0	295	2	Aaw82588 Human ATG
3	1487	100.0	295	2	Aaw49082 Homo sapi
4	1487	100.0	295	2	Aay06923 Human sec
5	1487	100.0	295	5	Abg31499 Human sec
6	1487	100.0	295	6	Abu55908 Human pro
7	1487	100.0	295	6	Aae34062 SARP 2 pr
8	1487	100.0	295	6	Abr47455 Breast Ca
9	1487	100.0	295	7	Adf77693 Human ful
10	1487	100.0	295	7	Adn40027 Cancer/an
11	1487	100.0	295	8	Adn05090 Antipsori
12	1487	100.0	295	8	Adr46694 Cancer-as
13	1483	99.7	295	2	Aay41748 Human PRO
14	1483	99.7	295	3	Aab44304 Human PRO
15	1483	99.7	295	5	Abb84861 Human PRO
16	1483	99.7	295	5	Abb95467 Human ang
17	1483	99.7	295	6	Abu25250 Novel hum
18	1483	99.7	295	6	Abu72256 Novel hum
19	1483	99.7	295	6	Abu84936 Human sec
20	1483	99.7	295	6	Abu61134 Human PRO
21	1483	99.7	295	6	Abu80403 Human sec
22	1483	99.7	295	6	Ada24954 Novel hum
23	1483	99.7	295	6	Abu19705 Novel hum
24	1483	99.7	295	6	Ada12615 Human sec
25	1483	99.7	295	6	Abu19596 Novel hum

RESULT 1  
ADf77694  
ID ADf77694 standard; protein; 275 AA.  
XX AC ADf77694;  
XX DT 26-FEB-2004 (first entry)  
XX DE Human mature Frazzled family protein SDF-5.

ALIGNMENTS

26	1483	99.7	295	7	ADB73921	Human PRO
27	1483	99.7	295	7	ADB76637	Human PRO
28	1483	99.7	295	7	ADC44063	Human sec
29	1483	99.7	295	7	ADC61823	Human sec
30	1483	99.7	295	7	ADC63787	Human sec
31	1483	99.7	295	7	ADC66887	Human sec
32	1483	99.7	295	7	ADC69011	Human sec
33	1483	99.7	295	7	ADC63071	Human sec
34	1483	99.7	295	7	ADC68136	Human sec
35	1483	99.7	295	7	ADC41456	Human sec
36	1483	99.7	295	7	ADC67511	Human sec
37	1483	99.7	295	7	ADC62447	Human sec
38	1483	99.7	295	7	ADC42080	Human sec
39	1483	99.7	295	7	ADD10379	Human sec
40	1483	99.7	295	7	ADD11339	Human sec
41	1483	99.7	295	7	ADD37132	Human sec
42	1483	99.7	295	7	ADE49449	Human sec
43	1483	99.7	295	7	ADE35503	Human sec
44	1483	99.7	295	7	ADE16617	Human sec
45	1483	99.7	295	7	ADD73232	Human sec

XX OS Homo sapiens.  
XX PN US2003175855-A1.  
XX PD 18-SEP-2003.  
XX PF 15-OCT-1997; 97US-00949904.  
XX PR 06-FEB-1997; 97US-00796153.  
XX PR 08-MAY-1997; 97US-00848439.  
XX PA (LAVA// LAVALLIE E R.  
XX PA (RACI// RACIE L A.  
XX PI Lavallie ER, Racie LA;  
XX PI WPI; 2003-898533/82.  
XX DR N-PSDB; ADf77692.  
XX PT New human SDF-5 DNA, useful for inducing formation, growth, differentiation, proliferation or maintenance of chondrocytes or cartilage tissues, or as nutritional sources or supplements.  
XX PS Claim 18; SEQ ID NO 3; 24pp; English.  
XX CC The invention relates to an isolated DNA sequence encoding mature or full length human SDF-5 (a frazzled family member) or its defined fragments, or which hybridises to it under stringent hybridisation conditions and encodes a protein that exhibits Frazzled activity. Also included are a vector comprising the above DNA molecule in operative association with an

CC expression control sequence, a host cell transformed with the vector, a  
CC method for producing purified human SDF-5 protein, a purified human SDF-5  
CC polypeptide, a composition comprising a therapeutic amount of at least  
CC one human SDF-5 polypeptide cited above, a method for altering the  
CC regulation of pancreatic genes in a patient (comprising administering to  
CC the patient an amount of the composition cited above), antibodies to a  
CC purified human SDF-5 protein and a method for increasing the  
CC differentiation of cells into chondrocytes, comprising applying a  
CC composition comprising BMP-2 (bone morphogenetic protein-2) and SDF-5.  
CC The DNA and protein are useful in regulating the binding of Wnt (wingnut)  
CC genes to their receptor or in inducing formation, growth,  
CC differentiation, proliferation and/or maintenance of chondrocytes and/or  
CC cartilage tissue, and for other tissue repair, such as pancreatic tissue  
CC repair. These may be used in the treatment of cartilage disorders, such  
CC as osteoarthritis, rheumatoid arthritis or articular cartilage defects.  
CC These may also be used for augmenting the activity of other tissue  
CC regenerating and differentiation factors. In addition, the protein and  
CC DNA are used as nutritional sources or supplements and in treating  
CC various immune deficiencies and disorders (e.g. infections, HIV,  
CC hepatitis, cancer, diabetes, inflammation or asthma) or neurological  
CC disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's  
CC disease). The present sequence represents mature human SDF-5.

XX Sequence 275 AA;

Query Match 100.0%; Score 1487; DB 7; Length 275;

Best Local Similarity 100.0%; Pred. No. 5.8e-138; Mismatches 0; Indels 0; Gaps 0;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
DB 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
QY 61 PLVMKQCHPDPTKFLCSLFAVPCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
DB 61 PLVMKQCHPDPTKFLCSLFAVPCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
QY 121 ECDRFPQDNDLCIPLASSDHLPPATEAPKVCYCKNKNDDNDIMETLCKNDFAKIKV 180  
DB 121 ECDRFPQDNDLCIPLASSDHLPPATEAPKVCYCKNKNDDNDIMETLCKNDFAKIKV 180  
QY 181 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
DB 181 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQ 275  
DB 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQ 275

RESULT 2

AAW82588

ID AAW82588 standard; protein; 295 AA.

XX AC AAW82588;

XX DT 01-MAR-1999 (first entry)

XX DE Human ATG-1622 protein.

XX KW ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;

XX KW diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;

XX KW heart disease; hypertension; kidney diseases; insulin resistance;

XX KW lipodystrophy; diabetes; central nervous system; CNS; gene mapping;

XX KW linkage analysis.

XX OS Homo sapiens.

XX PN EP879887-A1.

XX PD 25-NOV-1998.

XX PF 14-MAY-1998; 98EP-00303809.

XX 21-MAY-1997; 97US-0047251P.  
PR 13-JUN-1997; 97US-00874156.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Hu E, Zhu Y;  
XX WPI; 1998-596879/51.  
DR N-PSDB; AAV69384.  
XX New human secreted protein ATG-1622 polypeptide and polynucleotide -  
XX useful as diagnostic reagents and for prevention and treatment of Central  
XX Nervous System diseases and diabetes.

Claim 11; Page 22-23; 28pp; English.

This sequence represents the human ATG-1622 protein which is related to  
human secreted ligands for 7-transmembrane receptors and similar to  
murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for  
diagnosing susceptibility to diseases by detecting mutations in the ATG-  
1622 gene and can diagnose diseases associated with ATG-1622 imbalance.  
The polypeptides can be used to screen for agonists and antagonists which  
can be used in treatment to activate or inhibit ATG-1622 activity. The  
ATG-1622 polypeptide can be administered directly or as a vaccine to  
inoculate against disease. Diseases which can be diagnosed, prevented or  
treated by the ATG-1622 polypeptide or polynucleotides include heart  
disease, hypertension, kidney diseases, obesity, insulin resistance,  
lipodystrophy, diabetes and central nervous system (CNS) diseases. The  
ATG-1622 polypeptide is also useful for mapping the gene to a chromosome,  
allowing gene inheritance to be studied through linkage analysis

XX Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 2; Length 295;

Best Local Similarity 100.0%; Pred. No. 6.4e-138;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
DB 21 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDPTKFLCSLFAVPCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
DB 81 PLVMKQCHPDPTKFLCSLFAVPCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQDNDLCIPLASSDHLPPATEAPKVCYCKNKNDDNDIMETLCKNDFAKIKV 180  
DB 141 ECDRFPQDNDLCIPLASSDHLPPATEAPKVCYCKNKNDDNDIMETLCKNDFAKIKV 200  
QY 181 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 240  
DB 201 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVMWLKDSLOQTCCEMNDINAPYLV 260  
QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQ 275  
DB 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQ 295

RESULT 3

AAW49082

ID AAW49082 standard; protein; 295 AA.

XX AC AAW49082;

XX DT 09-NOV-1998 (first entry)

XX DE Homo sapiens SDF-5 protein.

XX KW SDF-5; frazzled; osteoarthritis; rheumatoid arthritis; cell formation;

XX KW proliferation; differentiation; diabetes; pancreatic cancer;

XX KW wound healing; gene therapy.

OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /note= "signal peptide"  
XX  
XX WO9835043-A1.  
XX  
XX 13-AUG-1998.  
XX  
XX 15-OCT-1997; 97WO-US018369.  
XX  
XX 06-FEB-1997; 97US-00796153.  
PR 08-MAY-1997; 97US-00848439.  
XX  
XX (GEMY ) GENETICS INST INC.  
XX  
XX Lavallie ER, Racie LA;  
PI WPI; 1998-447240/38.  
XX N-PSDB; AAV32930.  
DR  
XX Isolated DNA encoding human SDF-5 protein - useful for controlling  
PT growth, differentiation etc. of cells, particularly of chondrocytes for  
PT treatment of arthritis etc., also pancreatic cells.  
XX  
XX Claim 18; Page 57-58; 69pp; English.  
XX  
XX The sequence is that of human SDF-5, a member of the Frazzled protein  
CC family. Cells transformed with a vector containing the sequence are used  
CC to regulate genes, particularly pancreatic genes, or in combination with  
CC bone morphogenic protein 2 (BMP2), to increase differentiation of  
CC progenitor cells into chondrocytes. The protein may be used to treat  
CC osteoarthritis, rheumatoid arthritis, or articular cartilage defects,  
CC also to increase/inhibit cell formation, growth, differentiation,  
CC proliferation and/or maintenance in many other organs or tissues, e.g.  
CC for prevention or treatment of pancreatic cancer, diabetes (by inducing  
CC de novo formation of islet cells), other tissue defects, also to improve  
CC healing of wounds and to increase survival of nervous system cells, e.g.  
CC in cases of transplants. The coding sequence can be used in gene therapy,  
CC and its fragments to detect related mRNA, while the protein is also used  
CC to generate antibodies, useful for affinity purification and as  
CC immunoassay reagents. Many other potential uses/activities for the gene  
CC and its encoded are contemplated but not exemplified, e.g. as cytokines,  
CC immuno-suppressants or immunostimulants, regulators of haematopoiesis, as  
CC fertility-control agents, haemostatic or thrombolytic agents, anti-  
CC inflammatory agents, antimicrobials, modulators of biorhythms and many  
CC more  
XX  
XX Sequence 295 AA;  
SQ  
Query Match 100.0%; Score 1487; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 6.4e-138;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
DB 21 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKKFLCSLFAPVCLDDDETTPQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
DB 81 PLVMKQCHPDTKKFLCSLFAPVCLDDDETTPQCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDNDIMETLCNKDNFALKIKV 180  
DB 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDNDIMETLCNKDNFALKIKV 200  
QY 161 KEITYINRDTKIILETSTKYIKLVGVSERDLKKSVLWKDSLOCTCEMNDINAPYLVM 240  
DB 201 KEITYINRDTKIILETSTKYIKLVGVSERDLKKSVLWKDSLOCTCEMNDINAPYLVM 260  
QY 241 GQKGGELVITSVKRWQKQREFKRSIRKQLC 275

Db 261 GQKGGELVITSVKRWQKQREFKRSIRKQLC 295  
RESULT 4  
AY06923  
ID AAY06923 standard; protein; 295 AA.  
XX  
XX AAY06923;  
XX  
XX 01-JUL-1999 (first entry)  
XX  
XX Human secreted protein ligand ATG-1622 polypeptide.  
DE  
XX Human; ATG-1622 polypeptide; secreted protein ligand; 7-TM receptor;  
KW frizzled family; heart disease; hypertension; kidney disease; obesity;  
KW insulin resistance; lipodystrophy; diabetes; CNS disease.  
XX  
XX Homo sapiens.  
OS  
XX CA2229436-A.  
XX  
XX 21-NOV-1998.  
XX  
XX 23-APR-1998; 98CA-02229436.  
XX  
XX 21-MAY-1997; 97US-0047251P.  
PR 13-JUN-1997; 97US-00874156.  
PR 20-MAR-1998; 98US-00044885.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Hu E, Zhu Y;  
XX WPI; 1999-244679/21.  
DR N-PSDB; AAX34662.  
XX  
XX New secreted protein ligand polypeptide (ATG-1622) of 7-TM (frizzled  
PT family) receptors, useful for diagnosis, prevention and treatment of  
PT obesity, lipodystrophy, hypertension and heart disease.  
XX  
XX Claim 11; Page 10-11; 42pp; English.  
XX  
XX This represents a human ATG-1622 polypeptide, a secreted protein ligand  
CC for 7-TM (frizzled family) receptors. ATG-1622 polypeptides and  
CC polynucleotides are useful for diagnosing a disease or susceptibility to  
CC a disease by determining the presence/absence of a mutation in the ATG-  
CC 1622 gene, and/or analysing for the presence or amount of ATG-1622  
CC expressed in the patient. ATG-1622 expressing cells can be used to treat  
CC identifying modulators of the polypeptide which are can be used for  
CC conditions associated with a lack or excess of ATG-1622 polypeptide.  
CC Diseases diagnosed, prevented or treated include heart disease,  
CC hypertension, kidney diseases, obesity, insulin resistance,  
CC lipodystrophy, diabetes and CNS diseases. ATG-1622 protein may be useful  
CC for treating or preventing the onset of obesity. ATG-1622 polypeptides  
CC are also useful for mapping genes to chromosomes, allowing gene  
CC inheritance to be studies through linkage analysis  
XX  
XX Sequence 295 AA;  
SQ  
Query Match 100.0%; Score 1487; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 6.4e-138;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
DB 21 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKKFLCSLFAPVCLDDDETTPQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
DB 81 PLVMKQCHPDTKKFLCSLFAPVCLDDDETTPQCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDNDIMETLCNKDNFALKIKV 180



XX 25-MAR-2002; 2002WO-GB001195.  
XX 23-MAR-2001; 2001GB-00007296.  
PR 23-MAR-2001; 2001GB-00007299.  
PR 17-APR-2001; 2001GB-00009346.  
XX (AXOR-) AXORDIA LTD.  
XX  
XX Andrews P, Walsh J, Gokhale P;  
XX WPI: 2003-092852/08.  
DR N-PSDB; ABX75335.  
XX  
PT Modulating the differentiation of embryonic stem cells by providing  
PT ligands which bind receptors in the Notch and Wnt pathways, useful for  
PT treating diseases such as Parkinson's, Huntington's, heart disease,  
PT diabetes and AIDS.  
XX  
PS Disclosure; Fig 82; 12lpp; English.  
XX  
XX The invention relates to modulating the differentiation of an embryonic  
CC stem cell, comprising: (a) providing a culture of embryonic stem cells;  
CC (b) providing at least one ligand or its active binding fragment, capable  
CC of binding its cognate receptor polypeptide expressed by the embryonic  
CC stem cell; (c) forming a culture comprising embryonic stem cells and the  
CC ligand; and (d) growing the cell culture. Also included are: (i)  
CC Modulating the differentiation of embryonic stem cells, comprising: (a)  
CC providing a cell transfected with a nucleic acid molecule selected from:  
CC (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic  
CC acid molecule that hybridises to the nucleic acid in (i), and which  
CC encodes a ligand capable of modulating embryonic stem cell  
CC differentiation, or capable of binding a Wnt receptor; or (iii) nucleic  
CC acid molecules which are degenerate as a result of the genetic code to  
CC the sequences of (i) or (ii); (b) forming a culture comprising the cell  
CC identified in (a) with an embryonic stem cell; and (c) growing the  
CC culture for the maintenance and/or differentiation of the embryonic stem  
CC cell; (2) Inhibiting the differentiation of embryonic stem cells,  
CC comprising: (a) providing at least one polypeptide or its active  
CC fragment, that are inhibitors of the Wnt signalling pathway; (b) forming  
CC a culture comprising the cell identified in (a) with an embryonic stem  
CC cell; and (c) growing the culture for the maintenance of embryonic stem  
CC cells in an undifferentiated state; or (3) Inhibiting the differentiation  
CC of embryonic stem cells, comprising: (a) providing a cell transfected  
CC with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt  
CC inhibitory polypeptide; (ii) a molecule which hybridises to the molecule  
CC of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;  
CC and (iii) nucleic acid molecules which are degenerate as a result of the  
CC genetic code to the sequences of (i) or (ii); (b) forming a culture  
CC comprising the cell identified in (a) with an embryonic stem cell; and  
CC (c) growing the culture for the maintenance of embryonic stem cells in an  
CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture  
CC obtainable by any of the methods cited above. The therapeutic cell of the  
CC present invention is useful in the treatment of an animal, preferably a  
CC human, comprising administering a cell composition comprising embryonic  
CC stem cells which have been induced to differentiate into at least one  
CC cell-type. The cell is also useful for the manufacture of a composition  
CC for use in treatment of diseases such as Parkinson's disease,  
CC Huntington's disease, motor neuron disease, heart disease, diabetes,  
CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired  
CC immunodeficiency syndrome). The present sequence is represents a Wnt or  
CC Notch pathway protein (i.e. a ligand for the method of the invention)  
XX  
SQ Sequence 295 AA;  
Query Match 100.0%; Score 1487; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 6.4e-138;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX 1 SARGLFLGQPDFSKYRKNCKPIPANLQCHGIEYQNNRLNLLGHETMKEVLEQAGAWI 60  
DB 21 SARGLFLGQPDFSKYRKNCKPIPANLQCHGIEYQNNRLNLLGHETMKEVLEQAGAWI 80

QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFWPDM 120  
DB |||||  
QY 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFWPDM 140  
DB |||||  
QY 121 ECDREPDNDLCIPLASSDHLPLPATEAPKVCCEAKKNKDDNDIMETLCKNDFAKIKV 180  
DB |||||  
QY 141 ECDREPDNDLCIPLASSDHLPLPATEAPKVCCEAKKNKDDNDIMETLCKNDFAKIKV 200  
DB |||||  
QY 181 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLDKSLQCTCEMNDINAPYLV 240  
DB |||||  
QY 201 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLDKSLQCTCEMNDINAPYLV 260  
DB |||||  
QY 241 GQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 275  
DB |||||  
QY 261 GQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 295  
DB |||||  
RESULT 7  
AAE34062  
ID AAE34062 standard; protein; 295 AA.  
XX AC AAE34062;  
XX DT 02-MAY-2003 (first entry)  
XX DE SARP 2 protein.  
XX KW Drug screening; toxicology assay; signalling pathway; SARP 2.  
XX OS Unidentified.  
XX PN WO200290992-A2.  
XX PD 14-NOV-2002.  
XX PF 29-APR-2002; 2002WO-GB001946.  
XX PR 04-MAY-2001; 2001GB-00011004.  
XX PA (AXOR-) AXORDIA LTD.  
XX PI Andrews P, Draper J, Walsh J;  
XX WPI: 2003-120579/11.  
XX N-PSDB: AAD52560.  
XX Identifying biologically active agents comprises cloning transfected  
PT cells into a cell array, exposing the array to an agent to be tested, and  
PT detecting signals generated by a reporter molecule as a result of  
XX exposure to the agent.  
PS Claim 16; Fig 76; 90pp; English.  
XX The present invention relates to a novel screening method which enables  
CC the identification of biologically active agents which mediate their  
CC effect through the activation of genes. The method involves providing a  
CC population of cells stably transfected with a nucleic acid encoding a  
CC reporter molecule, cloning the transfected cells into a cell array,  
CC exposing the array to at least one agent to be tested and detecting a  
CC signal generated by the reporter molecule as a result of exposure to the  
CC agent. The method is useful in identifying biologically active agents and  
CC the genes through which the agents act, in screening potential drugs for  
CC their ability to activate certain drug targets in a high-throughput  
CC assay, in identifying relationships between signalling pathways and  
CC specific signals that could be useful in eventually directing the  
CC differentiation of embryonic stem cells and in toxicology assays by  
CC testing for unwanted activation or inhibition of specific signalling  
CC pathways. The present sequence is SARP 2 protein used to illustrate the  
CC method of the invention  
XX  
SQ Sequence 295 AA;  
Query Match 100.0%; Score 1487; DB 6; Length 295;

Best Local Similarity 100.0%; Pred. No. 6.4e-138;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SARGFLFLFGQPDFSKYKSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
Db 21 SARGFLFLFGQPDFSKYKSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
Qy 61 PLVMKQCHPDTKKFLCSLFPAPVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
Db 81 PLVMKQCHPDTKKFLCSLFPAPVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
Qy 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVEACEKNKDDNDIMETLCKNDPALKIKV 180  
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVEACEKNKDDNDIMETLCKNDPALKIKV 200  
Qy 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWKDSLQCTCEEMNDINAPYLVM 240  
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWKDSLQCTCEEMNDINAPYLVM 260  
Qy 241 GOKOGGELVITSVKRWQKGQREFKRSIRSKLQOC 275  
Db 261 GOKOGGELVITSVKRWQKGQREFKRSIRSKLQOC 295

RESULT 8  
ABR47455  
ID ABR47455 standard; protein; 295 AA.  
AC ABR47455;  
DT 12-JUN-2003 (first entry)  
DE Breast cancer associated protein sequence SEQ ID NO:142.  
KW Human; breast cancer; cytostatic; gene therapy.  
OS Homo sapiens.  
XX WO2003004989-A2.  
PN 16-JAN-2003.  
PD 21-JUN-2002; 2002WO-US019669.  
PF 21-JUN-2001; 2001US-0299887P.  
PR 27-JUN-2001; 2001US-0301572P.  
PR 18-JUL-2001; 2001US-0306501P.  
PR 25-SEP-2001; 2001US-0325002P.  
PR 05-MAR-2002; 2002US-0362585P.  
PR 14-MAY-2002; 2002US-0380391P.

(MILL-) MILLENIUM PHARM INC.  
PA Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;  
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
PI Bast RC, Hortobagyi GN, Fuszta L, Meric F, Sahin A, Mills GB;  
XX WPI; 2003-210381/20.  
DR N-PSDB; ACC50147.  
XX Breast cancer diagnosis or treatment by comparing the level of expression  
PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.  
XX Claim 1; SEQ ID NO 142; 128pp; English.  
PS The present invention describes a method for assessing whether a patient  
CC is afflicted with breast cancer. The method comprises comparing the level  
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
CC ABR47386 to ABR47632) in a patient sample and the normal level of  
CC expression of the marker in a control non-breast cancer sample, where a  
CC significant increase in the level of expression of the marker in the  
CC patient sample and the normal level is an indication that the patient is

CC afflicted with breast cancer. The breast cancer associated sequences from  
CC the present invention have cytostatic activities and can be used in gene  
CC therapy. The method is useful for diagnosing and treating breast cancer.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 295 AA;  
Query Match 100.0%; Score 1487; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 6.4e-138;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SARGFLFLFGQPDFSKYKSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
Db 21 SARGFLFLFGQPDFSKYKSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
Qy 61 PLVMKQCHPDTKKFLCSLFPAPVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
Db 81 PLVMKQCHPDTKKFLCSLFPAPVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
Qy 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVEACEKNKDDNDIMETLCKNDPALKIKV 180  
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVEACEKNKDDNDIMETLCKNDPALKIKV 200  
Qy 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWKDSLQCTCEEMNDINAPYLVM 240  
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWKDSLQCTCEEMNDINAPYLVM 260  
Qy 241 GOKOGGELVITSVKRWQKGQREFKRSIRSKLQOC 275  
Db 261 GOKOGGELVITSVKRWQKGQREFKRSIRSKLQOC 295  
RESULT 9  
ADF77693  
ID ADF77693 standard; protein; 295 AA.  
AC ADF77693;  
XX 26-FEB-2004 (first entry)  
DT Human full length Frazzled family protein SDF-5.  
DE Human; Frazzled family protein; SDF-5; pancreatic gene;  
KW chondrocyte differentiation; cartilage tissue formation; tissue repair;  
KW pancreatic tissue repair; cartilage disorders; osteoarthritis;  
KW rheumatoid arthritis; articular cartilage defect; nutritional source;  
KW nutritional supplement; immune deficiency; infection; HIV infection;  
KW hepatitis; cancer; diabetes; inflammation; asthma; neurological disorder;  
KW Parkinson's disease; Alzheimer's disease; Huntington's disease.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..20 /note= "Signal peptide"  
FT Region 18..295 /note= "Claimed in claim 2"  
FT Region 19..295 /note= "Claimed in claim 2"  
FT Region 20..295 /note= "Claimed in claim 2"  
FT Region /note= "Claimed in claim 2"  
FT Protein 21..295 /label= "Mature SDF\_5"  
FT /note= "Claimed in-claim 2"  
FT Region 22..295 /note= "Claimed in claim 2"  
FT Region 23..295 /note= "Claimed in claim 2"  
FT Region 24..295 /note= "Claimed in claim 2"  
FT Region 25..295 /note= "Claimed in claim 2"



FT	US2003175855-A1.	/note= "Claimed in claim 2"	
XX	18-SEP-2003.		
XX	15-OCT-1997; 97US-00949904.		
XX	06-FEB-1997; 97US-00796153.		
PR	08-MAY-1997; 97US-00848439.		
XX	(LAVA/) LAVALLIE E R.		
PA	(RACI/) RACIE L A.		
XX	Lavallie ER, Racie LA;		
XX	WPI: 2003-898533/82.		
DR	N-PSDB; ADP77692.		
XX	New human SDF-5 DNA, useful for inducing formation, growth, differentiation, proliferation or maintenance of chondrocytes or cartilage tissues, or as nutritional sources or supplements.		
PT	Claim 18; SEQ ID NO 2; 24pp; English.		
XX	The invention relates to an isolated DNA sequence encoding mature or full length human SDF-5 (a frazzled family member) or its defined fragments, or which hybridises to it under stringent hybridisation conditions and encodes a protein that exhibits Frazzled activity. Also included are a vector comprising the above DNA molecule in operative association with an expression control sequence, a host cell transformed with the vector, a method for producing purified human SDF-5 protein, a purified human SDF-5 polypeptide, a composition comprising a therapeutic amount of at least one human SDF-5 polypeptide cited above, a method for altering the regulation of pancreatic genes in a patient (comprising administering to the patient an amount of the composition cited above), antibodies to a purified human SDF-5 protein and a method for increasing the differentiation of cells into chondrocytes, comprising applying a composition comprising BMP-2 (Bone morphogenetic protein-2) and SDF-5. The DNA and protein are useful in regulating the binding of Wnt (wingnut) genes to their receptor or in inducing formation, growth, differentiation, proliferation and/or maintenance of chondrocytes and/or cartilage tissue, and for other tissue repair, such as pancreatic tissue repair. These may be used in the treatment of cartilage disorders, such as osteoarthritis, rheumatoid arthritis or articular cartilage defects. These may also be used for augmenting the activity of other tissue regenerating and differentiation factors. In addition, the protein and DNA are used as nutritional sources or supplements and in treating various immune deficiencies and disorders (e.g. infections, HIV, hepatitis, cancer, diabetes, inflammation or asthma) or neurological disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's disease). The present sequence represents full length human SDF-5.		
XX	Sequence 295 AA;		
SQ	Query Match Best Local Similarity 100.0%; Score 1487; DB 7; Length 295; Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 SARGLFLFGQDPFSYKRSNCKPFPANLQLCHGIEYQNNRPNLLGHETMKEVLEQAGAWI 60		
Db	21 SARGLFLFGQDPFSYKRSNCKPFPANLQLCHGIEYQNNRPNLLGHETMKEVLEQAGAWI 80		
QY	61 PLVMKQCHPDTKKFLCSLPAPVCLDDLETIPCHSLCVQVKRCAPVMSAFGFPWMDL 120		
Db	81 PLVMKQCHPDTKKFLCSLPAPVCLDDLETIPCHSLCVQVKRCAPVMSAFGFPWMDL 140		
QY	121 ECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKDDNDIMETLCRNDPALKTKV 180		
Db	141 ECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKDDNDIMETLCRNDPALKTKV 200		
QY	181 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLKDSLQCTCEBMDINAPYLV 240		
Db	201 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLKDSLQCTCEBMDINAPYLV 260		
QY	241 GQKGGELVITSVKRWQKGQREFKRSIRKJQC 275		
Db	261 GQKGGELVITSVKRWQKGQREFKRSIRKJQC 295		
RESULT 10			
ADN40027			
ID	ADN40027 standard; protein; 295 AA.		
XX	AC ADN40027;		
XX	DT 17-JUN-2004 (first entry)		
XX	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.		
DE	Human; differential expression; cancer; angiogenic disorder;		
XX	KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;		
KW	inflammatory disease; autoimmune disease;		
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;		
KW	detection; diagnosis; prognosis; drug screening; drug targeting;		
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;		
KW	vulnerary; Gene therapy; vaccine.		
XX	Homo sapiens.		
OS	WO2003042661-A2.		
PN	22-MAY-2003.		
XX	13-NOV-2002; 2002WO-US036810.		
PF	13-NOV-2001; 2001US-0350666P.		
XX	21-NOV-2001; 2001US-0332464P.		
PR	29-NOV-2001; 2001US-0334393P.		
PR	03-DEC-2001; 2001US-0335394P.		
PR	14-DEC-2001; 2001US-0340376P.		
PR	08-JAN-2002; 2002US-0347211P.		
PR	10-JAN-2002; 2002US-0347349P.		
PR	08-FEB-2002; 2002US-0355250P.		
PR	13-FEB-2002; 2002US-0356714P.		
PR	20-FEB-2002; 2002US-0359077P.		
PR	29-MAR-2002; 2002US-0368809P.		
PR	04-APR-2002; 2002US-0370110P.		
PR	12-APR-2002; 2002US-0372246P.		
PR	05-JUN-2002; 2002US-0386614P.		
PR	16-JUL-2002; 2002US-0396839P.		
PR	22-JUL-2002; 2002US-0397757P.		
PR	22-JUL-2002; 2002US-0397845P.		
PR	09-SEP-2002; 2002US-0409450P.		
XX	(EOSB-) EOS BIOTECHNOLOGY INC.		
PA	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;		
PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;		
PI	WPI; 2003-468649/44.		
XX	N-PSDB; ADN39810.		
DR	Determining the presence or absence of a pathological cell in a patient,		
PT	useful for diagnosing, prognosing or treating cancer, comprises detecting		
PT	a nucleic acid in a biological sample.		
XX	Claim 12; SEQ ID NO C397; 1385pp; English.		
PS	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)		
CC	whose expression is upregulated or downregulated in specific cancers or		
CC	other diseases such as angiogenic or fibrotic disorders, and to methods		
CC	of determining the presence or absence of a pathological cell in a		
CC	patient by detecting a nucleic acid at least 80% identical to those of		
CC	the invention or by detecting a polypeptide of the invention. The		
CC	invention also relates to expression vectors and host cells comprising a		

CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndrome, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX  
SQ Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 7; Length 295;

Best Local Similarity 100.0%; Pred. No. 6.4e-138;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60

Db 21 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80

QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKRCAPVMSAFGFPWPDML 120

Db 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKRCAPVMSAFGFPWPDML 140

QY 121 ECDRFPQNDLICIPLASSDHLIPATEAPKVCEACKNKNDDNDIMETLCKNDFALKIKV 180

Db 141 ECDRFPQNDLICIPLASSDHLIPATEAPKVCEACKNKNDDNDIMETLCKNDFALKIKV 200

QY 181 KEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWKDSLOCTCEEMNDINAPYLVM 240

Db 201 KEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWKDSLOCTCEEMNDINAPYLVM 260

QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275

Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295

RESULT 11

ADN05090

ID ADN05090 standard; protein; 295 AA.

AC ADN05090;

XX 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #724.

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH ) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu TD;

XX WPI; 2004-305105/28.

DR N-PSDB; ADN05089.

XX New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.

PS Claim 9; SEQ ID NO 1484; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention.

XX Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 8; Length 295;

Best Local Similarity 100.0%; Pred. No. 6.4e-138;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60

Db 21 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80

QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKRCAPVMSAFGFPWPDML 120

Db 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKRCAPVMSAFGFPWPDML 140

QY 121 ECDRFPQNDLICIPLASSDHLIPATEAPKVCEACKNKNDDNDIMETLCKNDFALKIKV 180

Db 141 ECDRFPQNDLICIPLASSDHLIPATEAPKVCEACKNKNDDNDIMETLCKNDFALKIKV 200

QY 181 KEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWKDSLOCTCEEMNDINAPYLVM 240

Db 201 KEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWKDSLOCTCEEMNDINAPYLVM 260

QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275

Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295

RESULT 12

ADR46694

ID ADR46694 standard; protein; 295 AA.

AC ADR46694;

XX 18-NOV-2004 (first entry)

XX Cancer-associated protein, SEQ ID 107.

KW Cytostatic; Gene Therapy; cancer; human.

XX Homo sapiens.

XX WO2004073657-A2.

XX 02-SEP-2004.

XX 19-FEB-2004; 2004WO-US005455.

XX 19-FEB-2003; 2003US-0448784P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Gish KC, Wilson KE, Zlotnik A;

XX WPI; 2004-652787/63.

DR N-PSDB; ADR46636.

XX Detecting a pathological cell in a patient for diagnosing or treating  
PT cancer by detecting in a biological sample from the patient genes whose  
PT expression are up-regulated or down-regulated in specific cancers.

PS Claim 1; SEQ ID NO 107; 375pp; English.

XX The present invention relates to a method for detecting cancer in a  
CC patient. The method comprises detecting in a biological sample from the  
CC patient a nucleotide or protein sequence comprising a sequence that is at  
CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or



DR N-PSDB; AAB434241.  
XX  
PT New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.  
XX  
PS  
PS Claim 12; Fig 167; 530pp; English.  
XX  
CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX  
XX Sequence 295 AA;  
SQ  
Query Match 99.7%; Score 1483; DB 2; Length 295;  
Best Local Similarity 99.6%; Pred. No. 1.6e-137;  
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
Db 21 SARGFLFGQDPFSYKRSNCKPIPVNLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKFKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
Db 81 PLVMKQCHPDTKFKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 180  
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 200  
QY 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240  
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260  
QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275  
Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295  
RESULT 14  
ID AAB44304  
XX AAB44304 standard; protein; 295 AA.  
XX  
AC AAB44304;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human PRO697 (UNQ361) protein sequence SEQ ID NO:415.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
KW expressed sequence tag; detection; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200053756-A2.  
XX  
PD 14-SEP-2000.  
XX  
XX 18-FEB-2000; 2000WO-US004341.  
XX  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 29-MAR-1999; 99US-0126773P.  
PR 21-APR-1999; 99US-0130232P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US028565.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
DR WPI; 2000-611443/58.  
DR N-PSDB; AAC78560.  
XX  
XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.  
XX  
PS Claim 12; Fig 167; 636pp; English.  
XX  
CC AACT78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytotstatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells; e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
SQ Sequence 295 AA;  
Query Match 99.7%; Score 1483; DB 3; Length 295;  
Best Local Similarity 99.6%; Pred. No. 1.6e-137;  
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60  
Db 21 SARGFLFGQDPFSYKRSNCKPIPVNLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKFKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFPWPDML 120  
Db 81 PLVMKQCHPDTKFKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFPWPDML 140  
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 180  
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 200  
QY 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240  
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260  
QY 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275  
Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295  
RESULT 15  
ID ABB84861  
XX ID ABB84861 standard; protein; 295 AA.  
XX

AC ABB84861;  
XX  
XX 16-MAY-2002 (first entry)  
XX  
XX Human PRO697 protein sequence SEQ ID NO:90.  
XX  
XX Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;  
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
XX Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US019692.  
XX  
XX 23-JUN-2000; 2000US-0213637P.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-0064610.  
PR 18-SEP-2000; 2000US-0065350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 30-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritson ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NP;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI; 2002-090516/12.  
DR N-PSDB; ABL88116.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 11; Fig 90; 565pp; English.  
PS

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention  
XX  
XX SQ Sequence 295 AA;  
Query Match 99.7%; Score 1483; DB 5; Length 295;  
Best Local Similarity 99.6%; Pred. No. 1.6e-137;  
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKVLEQAGAWI 60  
DB 21 SARGLFLFGQDPFSYKRSNCKPIPVNLQCHGIEYQNMRLPNLLGHETMKVLEQAGAWI 80  
QY 61 PLVMKQCHPDTKKFLCSLFAVCLDDLDDETIQPCHSCLCVQVKDRCAPVMSAFGPPWDM 120  
DB 81 PLVMKQCHPDTKKFLCSLFAVCLDDLDDETIQPCHSCLCVQVKDRCAPVMSAFGPPWDM 140  
QY 121 ECDRFPQDNDLCIPLASSDHLHPATEAPKVCCKNKNDDDDNDIMETLCKNDPALKIKV 180  
DB 141 ECDRFPQDNDLCIPLASSDHLHPATEAPKVCCKNKNDDDDNDIMETLCKNDPALKIKV 200  
QY 181 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVLWLDKSLQCTCEEMNDINAPYLVM 240  
DB 201 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVLWLDKSLQCTCEEMNDINAPYLVM 260  
QY 241 GQKGGELVITSVKRWKGQREFKRSIRSKLQ 275  
DB 261 GQKGGELVITSVKRWKGQREFKRSIRSKLQ 295

Search completed: September 1, 2005, 10:50:29  
Job time : 112.412 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:17:03 ; Search time 26.3947 Seconds  
(without alignments)  
1075.364 Million cell updates/sec

Title: US-08-949-904A-2  
Perfect score: 1594  
Sequence: 1 MLQPGSLLLLFLASHCCLG.....WQKGQREFKRISIRKLQC 295

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	2 JE0174	frizzled protein-2
2	616.5	38.7	317	2 JE0175	frizzled protein-1
3	279.5	17.5	537	2 JC7127	frizzled protein 4
4	272.5	17.1	568	2 T25162	Frizzled-1 protein
5	269	16.9	581	2 JC7086	FZD10 protein - hu
6	269	16.9	647	2 JE0337	Frizzled-1 protein
7	267.5	16.8	550	2 T37325	wingless protein r
8	264.5	16.6	574	2 JE0339	Frizzled-7 protein
9	262	16.4	565	2 JE0338	Frizzled-2 protein
10	259.5	16.3	641	2 A45054	probable intercell
11	241	15.1	694	2 S71786	wingless receptor
12	224.5	14.1	605	2 T31690	hypothetical prote
13	223	14.0	581	2 S03540	gene frizzled prot
14	220.5	13.8	1113	2 JE0315	low-density lipopr
15	216.5	13.6	666	2 JC7312	frizzled-3 protein
16	213.5	13.4	197	2 JC7735	frizzled-related p
17	205	12.9	706	2 JE0164	frizzled-6 protein
18	177.5	11.1	579	2 JC7629	membrane-type friz
19	152.5	9.6	1774	2 B56101	collagen alpha 1(X
20	133.5	8.4	526	2 T13484	frizzled protein h
21	119	7.5	581	2 B54665	netrin-2 precursor
22	100	6.3	793	2 JC5539	Smoothed protein
23	98.5	6.2	1342	2 A36223	kinase-related tra
24	95.5	6.0	1282	2 JE0120	glycoprotein A m
25	93.5	5.9	1339	2 JC4387	epidermal growth f
26	92.5	5.8	495	2 B70322	hypothetical prote
27	91	5.7	532	2 AE1964	Dnak-type molecula
28	91	5.7	1290	2 A55094	chromosomal protei
29	89.5	5.6	392	2 E81325	probable dihydroor

ALIGNMENTS

RESULT 1

JE0174  
frizzled protein-2 - human  
C:Species: Homo sapiens (man)  
C>Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JE0174  
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998  
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.  
A:Reference number: JE0174; MUID:98308108; PMID:9642118  
A:Accession: JE0174  
A:Molecule type: mRNA  
A:Residues: 1-295 <HUA>  
A:Cross-references: UNIPROT:Q9HAP5  
C:Genetics:  
A:Map position: 4q

Query Match 100.0%; Score 1594; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1e-118;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQPGSLLLLFLASHCCLGSLFQGPDPDFSYKRSNCKPPIANLQCHGIEYQNNRL	60
Db	1	MLQPGSLLLLFLASHCCLGSLFQGPDPDFSYKRSNCKPPIANLQCHGIEYQNNRL	60
Qy	61	PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKFLCSLFAPVCLDDLDDETIQPCHSVCVQ	120
Db	61	PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKFLCSLFAPVCLDDLDDETIQPCHSVCVQ	120
Qy	121	VKDRCAPVMSAFGFPWDMLECDRPPQNDLCIPLASSDHLPPATEAPKVCACKNNKD	180
Db	121	VKDRCAPVMSAFGFPWDMLECDRPPQNDLCIPLASSDHLPPATEAPKVCACKNNKD	180
Qy	181	DDNDIMETLCKNDPALKIKVKEIYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK	240
Db	181	DDNDIMETLCKNDPALKIKVKEIYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK	240
Qy	241	DSLQCTCEEMNDINAPVLMQKQGGELVITSVKRWQKGQREFKRISIRKLQC	295
Db	241	DSLQCTCEEMNDINAPVLMQKQGGELVITSVKRWQKGQREFKRISIRKLQC	295

RESULT 2

JE0175  
frizzled protein-1b - human  
C:Species: Homo sapiens (man)  
C>Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JE0175  
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998  
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.  
A:Reference number: JE0174; MUID:98308108; PMID:9642118

A;Accession: JE0175  
A:Molecule type: mRNA  
A;Residues: 1-317 <HUA>  
A;Cross-references: UNIPROT:O14780  
C;Genetics:  
A;Gene: hPRP-1b  
A;Map position: 5q14.3-q12.1

Query Match 38.7%; Score 616.5; DB 2; Length 317;  
Best Local Similarity 43.9%; Pred. No. 2.3e-41;  
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 7 SLLLLFLASHCCGLSGARGFLFLFG-OPDFSYKESNCKP-----IPANLQLCHEGYQNNRL 60  
DB 14 ALALLGALHWPARCEEVHYGWAQEPHLGRYSKPPQCLDIPADLPCHTGVGYKMR 73  
QY 61 PNLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSLSVQ 120  
DB 74 PNLHEHSLAEVKQASSWLPALLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLCEA 130  
QY 121 VKDCAPVMSAFGFPWPMLECDRPPQNDLICIPLASSDHLHPATEAP---KVCEACKN 177  
DB 131 VRAGCAPLMEAYGFPWPMLECHKFPDNDLCLIAVQFGH--LPAT--APPVTKICAQCEM 186  
QY 178 KNDNDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVL 237  
DB 187 EHSADG-LMEQCCSDFVVMRIKEIKTIENGDRKLIGAQKKKKLLKPLGPKRKOTKRLVL 245  
QY 238 WLKDSLQTCCEEMNDINAPLVMGQKGGELVITSVKRWQKQREBFK 284  
DB 246 HMKNGAGCPCPLDLSLGSFLVWGRKVDGQLLLMAYVRWDKKNKEMK 292

RESULT 3  
JC7127  
frizzled protein 4 - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
A;Accession: JC7127  
R;Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.  
Biochem. Biophys. Res. Commun. 264, 955-961, 1999  
A;Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-  
A;Reference number: JC7127; MUID:20012777; PMID:10544037  
A;Accession: JC7127  
A;Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-537 <KIR>  
A;Cross-references: UNIPROT:Q9ULV1; GB:AB032417; DBJ:AB032417; NID:g6277265; PID:g62772  
C;Genetics:  
A;Gene: FZD4  
A;Map position: 11 region q14 - q21  
C;Superfamily: fruit fly frizzled protein

Query Match 17.5%; Score 279.5; DB 2; Length 537;  
Best Local Similarity 31.4%; Pred. No. 1.9e-14;  
Matches 69; Conservative 30; Mismatches 90; Indels 31; Gaps 8;

QY 4 GPGSLLLFLASHCCGLSGARGFLFLFG-PDFSYKRSNCKPPIPANLQLCHEGYQNNRLPNL 63  
DB 16 GVGLSLGLLLQLLLGLPARG---FGDEE---ERRCDPI--RISMCCNLGYNVTKPNL 66  
QY 64 LGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSLSVQKD 123  
DB 67 VGHLEQTDALQLJTFTPLTIQVGCSSQLQFLCSYVPMCTEKNINIPGCGMCLSVKR 126  
QY 124 RCAPVMSAFGFPWPMLECDRPPQND---LC-----IPLASSDHLHPATEAPKVC 172  
DB 127 RCEPLVKFGFAPWPSLNCSEKFPQNDHNMCMGEGDEEPLPKHTPIQCEE-----C 181  
QY 173 EACKNKNDNDIMETL-----CKNDFALKIK-VKEITYI 206  
DB 182 HSVGNTSQDIYIWKRSNLKCVLKGCGYDAGLYSRSAKEFTDI 221

## RESULT 4

T25162  
Frizzled-1 protein homolog - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T25162; T42210  
R;Wild, A.

submitted to the EMBL Data Library, October 1996  
A;Reference number: Z19989

A;Accession: T25162

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Residues: 1-568 <WIL>

A;Cross-references: UNIPROT:O16147; EMBL:Z81128; PIDN:CAB03398.1; GSPDB:GN000019; CESP:T2

R;Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie

Cell 90, 707-716, 1997

A;Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embr

A;Reference number: Z15051; MUID:97433081; PMID:9288750

A;Accession: T42210

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-568 <ROC>

A;Cross-references: EMBL:AF013953; NID:g2463673; PIDN:AAC47750.1; PID:g2463674

C;Genetics:

A;Gene: mom-5; T23D8.1

A;Map position: 1

A;Introns: 158/2; 280/1; 326/2; 407/1; 447/2; 520/2

C;Superfamily: fruit fly frizzled protein

Query Match 17.1%; Score 272.5; DB 2; Length 568;

Best Local Similarity 29.3%; Pred. No. 7.4e-14;

Matches 73; Conservative 38; Mismatches 97; Indels 41; Gaps 9;

QY 8 LLLFLASHCCGLSGARGL---FLFGPDFSYKRSNCKPPIPANLQLCHEGYQNNRLPNLL 64  
DB 5 LLILFLFG--CLSDAQLSSTSISMMNGFSTR-KCHEI--TIPCKNLDTNQTFFNLL 59  
QY 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSLSVQKDR 124  
DB 60 GHTTQSEAGPAIAQFNPLIKVKCEDIRLFLCTVYAPVC-TVLEKPIQPCRELCLSAKNG 118  
QY 125 CAPVMSAFGFPWPMLECDRPPQNDLICIPLASSDHLHPATEAPKVCCEACKNKNDND 184  
DB 119 CESLMKKFGFQWPDQCNKFPV-TDLCVGNKNSSE-----SSNSKKSND 162  
QY 185 IMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLQ 244  
DB 163 V-----TFGVSTIANEVVLSPKKCPHHMTTSGSHFSLPLLSGRLPESCL----- 207  
QY 245 CTCEEMNDI 253  
DB 208 -TCEADNQV 215

## RESULT 5

JC7086

FZD10 protein - human

C;Species: Homo sapiens (man)

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: JC7086

R;Koike, J.; Takagi, A.; Miwa, T.; Hirai, M.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 262, 39-43, 1999

A;Title: Molecular cloning of Frizzled-10, a novel member of the Frizzled gene family.

A;Reference number: JC7086; MUID:99382237; PMID:10448064

A;Accession: JC7086

A:Molecule type: mRNA

A;Residues: 1-581 <KOI>

A;Cross-references: UNIPROT:Q9ULW2; DBJ:AB027464; NID:g5834487; PIDN:BAA84093.1; PID:g5

A;Experimental source: fetal lung

C;Genetics:

A;Gene: Frizzled-10 (fzd-10)





QY 8 LLLLFLASHCCLSGARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMPLNLGHE 67  
Db 14 LLLLPAAGPAQFHGXGISI---PDHGF---CQPI--SIPLCTDIAYNTQTIMPLNLGHT 64

QY 68 TMKEVLEQAGAWIPLVMKQCHPTDKKFLCSLFAPVCLDDLETIQPCHSLCVQVKDRCAP 127  
Db 65 NQEDAGLEVHQFVPLVKVQCSFELRFLCSMTAPVC-TVLEQAIPPCRSICERARQGCEA 123

QY 128 VNSAFGFPWDMLECDRFPQD--NDLCIPLASSDHLPLA 164  
Db 124 LMKFGQFWPERLRCEHFFRHGAEQICVGNHSEDGAPA 162

RESULT 10  
A45054  
probable intercellular signal transducer or transmitter Fz-1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 02-Mar-2001  
C:Accession: A45054  
R:Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992  
A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed  
A:Reference number: A45054; MUID:93094228; PMID:1334084  
A:Accession: A45054  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-641 <CHA>  
A:Experimental source: UMR 106 osteosarcoma cell line  
A>Note: sequence extracted from NCBI backbone (NCBIP:120154)  
C:Superfamily: fruit fly frizzled protein

Query Match 16.3%; Score 259.5; DB 2; Length 641;  
Best Local Similarity 37.3%; Pred. No. 9.1e-13;  
Matches 56; Conservative 27; Mismatches 54; Indels 13; Gaps 6;

QY 23 RGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPL 82  
Db 101 RGISI---PDHGY---CQPI--SIPLCTDIAYNTQTIMPLNLGHTNQEDAGLEVHQFVPL 151

QY 83 VMKQCHPTDKKFLCSLFAPVCLDDLETIQPCHSLCVQVKDRCAPVMSAFGFPWDMLEC 142  
Db 152 VKVQCSAELKFFLCSMTAPVC-TVLEQALPPCRSLCERAOQ-CEALMNKFGFQWPDTLKC 209

QY 143 DRFPQD--NDLCIPLASSDHLPLATEAPK 170  
Db 210 EKFPVHGRGELCVGQNTSDKGTPTPSLLPE 239

RESULT 11  
S71786  
wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: S71786; S78444  
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; Andrew, Nature 382, 225-230, 1996  
A:Title: A new member of the frizzled family from Drosophila functions as a wingless rec  
A:Reference number: S71786; MUID:96353971; PMID:8717036  
A:Accession: S71786  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-694 <BHA>  
A:Cross-references: UNIPROT:O9VVX3; EMBL:U65589  
A>Note: mRNA was also sequenced  
R:Bhanot, P.; Wang, Y.; Nathans, J.  
submitted to the EMBL Data Library, July 1996  
A:Reference number: S78444  
A:Accession: S78444  
A:Molecule type: DNA  
A:Residues: 1-416, T', 418-694 <BHW>  
A:Cross-references: EMBL:U65589; NID:g1518050; PIDN:AAC47273.1; PID:g1518051  
C:Genetics:

A:Gene: dfz2  
A:Cross-references: FlyBase:FBgn0016797  
C:Superfamily: fruit fly frizzled protein  
C:Keywords: transmembrane protein

Query Match 15.1%; Score 241; DB 2; Length 694;  
Best Local Similarity 35.3%; Pred. No. 2.9e-11;  
Matches 49; Conservative 20; Mismatches 50; Indels 20; Gaps 5;

QY 40 CKPIPANLQCHGIEYQNMRLPNLLGHETMKEV-LEQAGAWIPLVMKQCHPTDKKFLCSL 98  
Db 64 CEEI--TIPMCRGIGYNNTSFPMNMHETQDEAGLEVHQFW-PLVEIKCSPLDKFLFLCSM 120

QY 99 PAPVCLDDLETIQPCHSLCVQVKDRCAPVMSAFGFPWDMLECDRFPQDND---LCIPL 155  
Db 121 YTPICLEDYHKPLPVCRCVCRARSGCAPINQQYSFEMPERMACHEHLPFHGDPDLNLCM-- 178

QY 156 ASSDHLPLATEAPKVCEA 174  
Db 179 -----EQPSYTEA 186

RESULT 12  
T31690  
hypothetical protein F27E11.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 02-Mar-2001  
C:Accession: T31690  
R:Wamsley, P.; Keppler, D.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid F27E11.  
A:Reference number: 221069  
A:Accession: T31690  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-605 <WAM>  
A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3  
A:Experimental source: strain Bristol N2; clone F27E11  
C:Genetics:  
A:Gene: CESP:F27E11.3  
A:Map position: 5  
A:Introns: 28/3; 454/1; 520/1; 562/1  
C:Superfamily: fruit fly frizzled protein

Query Match 14.1%; Score 224.5; DB 2; Length 605;  
Best Local Similarity 33.3%; Pred. No. 5e-10;  
Matches 42; Conservative 27; Mismatches 50; Indels 7; Gaps 2;

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPTDKKFLCSLFAPVCLDDLETIQPCHSLCVQ 120  
Db 5 PNSYGHKQBEAGLEVHQFVPLVEVGCFOHLKFFLCTWYTPICOENYDKPLPLCMELCVE 64

QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEAPKVCEA---CKN 177  
Db 65 ARSKCSPIMAKYGFRWETLSCEALPKMSD-----QMSTGNICAAAPDPTPKKQKHGHHKN 120

QY 178 KNDDDN 183  
Db 121 QNQNQN 126

RESULT 13  
S03540  
gene frizzled protein precursor - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C:Accession: S03540; S15708; S15709  
R:Vinson, C.R.; Conover, S.; Adler, P.N.  
Nature 338, 263-264, 1989  
A:Title: A Drosophila tissue polarity locus encodes a protein containing seven potential  
A:Reference number: S03540; MUID:89159415; PMID:2493583  
A:Accession: S03540  
A>Status: not compared with conceptual translation



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:54:34 ; Search time 114.895 Seconds  
(without alignments)  
1011.168 Million cell updates/sec

Title: US-08-949-904A-2

Perfect score: 1594

Sequence: 1 MLQGFGLLLFLASHCLIG.....WKGQREFKRISIRKLQC 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	8	US-08-949-904-2
2	1594	100.0	295	14	US-10-177-293-142
3	1594	100.0	295	15	US-10-295-027-1345
4	1594	100.0	295	16	US-10-783-528-107
5	1594	100.0	295	17	US-10-847-972-78
6	1594	100.0	295	17	US-10-432-256-2
7	1590	99.7	295	9	US-09-978-293A-415
8	1590	99.7	295	9	US-09-978-697-415
9	1590	99.7	295	9	US-09-978-192A-415
10	1590	99.7	295	9	US-09-999-832A-415
11	1590	99.7	295	10	US-09-978-189-415

12	1590	99.7	295	10	US-09-978-608A-415
13	1590	99.7	295	10	US-09-978-585A-415
14	1590	99.7	295	10	US-09-978-191A-415
15	1590	99.7	295	10	US-09-978-403A-415
16	1590	99.7	295	10	US-09-978-564A-415
17	1590	99.7	295	10	US-09-999-833A-415
18	1590	99.7	295	10	US-09-981-915A-415
19	1590	99.7	295	10	US-09-978-824-415
20	1590	99.7	295	10	US-09-918-855A-415
21	1590	99.7	295	10	US-09-999-834A-415
22	1590	99.7	295	10	US-09-978-423A-415
23	1590	99.7	295	10	US-09-978-193A-415
24	1590	99.7	295	10	US-09-999-830A-415
25	1590	99.7	295	10	US-09-978-757A-415
26	1590	99.7	295	10	US-09-978-187B-415
27	1590	99.7	295	10	US-09-978-643A-415
28	1590	99.7	295	10	US-09-978-375A-415
29	1590	99.7	295	10	US-09-978-298A-415
30	1590	99.7	295	10	US-09-978-188A-415
31	1590	99.7	295	10	US-09-978-681A-415
32	1590	99.7	295	10	US-09-978-194A-415
33	1590	99.7	295	10	US-09-999-829A-415
34	1590	99.7	295	10	US-09-978-299A-415
35	1590	99.7	295	10	US-09-978-544A-415
36	1590	99.7	295	10	US-09-978-665A-415
37	1590	99.7	295	10	US-09-978-802A-415
38	1590	99.7	295	11	US-09-999-831A-415
39	1590	99.7	295	12	US-09-978-824-415
40	1590	99.7	295	14	US-10-017-081A-415
41	1590	99.7	295	14	US-10-167-749-415
42	1590	99.7	295	14	US-10-013-921A-415
43	1590	99.7	295	14	US-10-013-929A-415
44	1590	99.7	295	14	US-10-016-177A-415
45	1590	99.7	295	14	US-10-223-085-90

ALIGNMENTS

RESULT 1  
US-08-949-904-2  
Sequence 2, Application US/08949904  
Publication No. US20030175855A1  
GENERAL INFORMATION:  
APPLICANT: Racie, Lisa  
APPLICANT: Lavallie, Edward  
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENETICS INSTITUTE, INC.  
STREET: 87 CAMBRIDGE PARK DRIVE  
CITY: CAMBRIDGE  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/949,904  
FILING DATE: October 15, 1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: LAZAR, STEVEN R.  
REGISTRATION NUMBER: 32,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8260  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-949-904-2

Query Match          100.0%; Score 1594; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
Db 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120

QY 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCCEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCCEACKNKND 180

QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240

QY 241 DSLOQTCBEMNDINAPYLVMGOKGGELVITSVKRWQKGQREFKRIISRIRKLOC 295
Db 241 DSLOQTCBEMNDINAPYLVMGOKGGELVITSVKRWQKGQREFKRIISRIRKLOC 295

RESULT 2
US-10-177-293-142
; Sequence 142, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumel
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 142
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-142

Query Match          100.0%; Score 1594; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
Db 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120

QY 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCCEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCCEACKNKND 180

QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240

QY 241 DSLOQTCBEMNDINAPYLVMGOKGGELVITSVKRWQKGQREFKRIISRIRKLOC 295
Db 241 DSLOQTCBEMNDINAPYLVMGOKGGELVITSVKRWQKGQREFKRIISRIRKLOC 295

RESULT 3
US-10-295-027-1345
; Sequence 1345, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1345  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-1345

Query Match 100.0%; Score 1594; DB 15; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.9e-139;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
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QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295  
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295

## RESULT 4

US-10-783-528-107  
; Sequence 107, Application US/10783528  
; Publication No. US20040219579A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha  
; APPLICANT: Gish, Kurt  
; APPLICANT: Wileon, Keith  
; APPLICANT: Zlorenik, Albert

; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND

; FILE REFERENCE: 05882.0191.NPUS01

; CURRENT APPLICATION NUMBER: US/10/783,528

; CURRENT FILING DATE: 2004-02-19

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 107

; LENGTH: 295

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-783-528-107

Query Match 100.0%; Score 1594; DB 16; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.9e-139;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
DB 1 MLOGPGSLLLLFLASHCCCLGSARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIOPCHSLCVQ 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIOPCHSLCVQ 120  
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240

QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295  
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295

## RESULT 5

US-10-847-972-78

; Sequence 78, Application US/10847972  
; Publication No. US20050049195A1

; GENERAL INFORMATION:

; APPLICANT: ZOU, YIMIN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION

; FILE REFERENCE: ARCD:395US

; CURRENT APPLICATION NUMBER: US/10/847,972

; CURRENT FILING DATE: 2004-05-17

; PRIOR APPLICATION NUMBER: 60/470,913

; PRIOR FILING DATE: 2003-05-15

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 78

; LENGTH: 295

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-847-972-78

Query Match 100.0%; Score 1594; DB 17; Length 295;

Best Local Similarity 100.0%; Pred. No. 1.9e-139;

Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLOGPGSLLLLFLASHCCCLGSARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIOPCHSLCVQ 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIOPCHSLCVQ 120  
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEACKNND 180  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295  
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKLCQ 295

## RESULT 6

US-10-432-256-2

; Sequence 2, Application US/10432256

; Publication No. US20050113291A1

; GENERAL INFORMATION:

; APPLICANT: Applied Research Systems ARS Holding N.V.

; TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma

; FILE REFERENCE: EP 469 Y

; CURRENT APPLICATION NUMBER: US/10/432,256

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 295

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-432-256-2

Query Match 100.0%; Score 1594; DB 17; Length 295;

Best Local Similarity 100.0%; Pred. No. 1.9e-139;

Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60







[illegible]

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.7%; Score 1590; DB 9; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQGGSLLLFLASHCCIGSARGLEFLGQPDFSYKRSNCKPVPANLQICHGIEYQNMRL 60
Db 1 MLQGGSLLLFLASHCCIGSARGLEFLGQPDFSYKRSNCKPVPANLQICHGIEYQNMRL 60
QY 61 PNLLGHETMKEVLEQAGWIPVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCHSLCQV 120
Db 61 PNLLGHETMKEVLEQAGWIPVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCHSLCQV 120
QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLPLATEAPKVCEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLPLATEAPKVCEACKNKND 180
QY 181 DNDIMETLCKNDFAIKVKEITYNIRDTKILLETKSTIYKLVGVSERDLKKSVMWLK 240
Db 181 DNDIMETLCKNDFAIKVKEITYNIRDTKILLETKSTIYKLVGVSERDLKKSVMWLK 240
QY 241 DLSQTCCEBMNDINAPYLVNGKQGGELVITSVKRWQKQREFKRISIRKLQC 295
Db 241 DLSQTCCEBMNDINAPYLVNGKQGGELVITSVKRWQKQREFKRISIRKLQC 295

RESULT 9
US-09-978-192A-415
; Sequence 415, Application US/09978192A
; Patent No. US20030177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9

; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
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; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR APPLICATION NUMBER: 60/085339  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 9; Length 295;

Best Local Similarity 99.7%; Pred. No. 4.4e-139;

Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLOGPGSILLFLASHCCLGSGARGLFLPGQDPDFSYKSNCKPIPANLQCHGIEYQNMRL 60  
Db 1 MLOGPGSILLFLASHCCLGSGARGLFLPGQDPDFSYKSNCKPIPVNLQCHGIEYQNMRL 60  
Qy 61 PNLLGHETMKEVLBOAGAWIPLVMKQCHPDPTKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120  
Db 61 PNLLGHETMKEVLBOAGAWIPLVMKQCHPDPTKFLCSLFAFVCLDDLDDETTQPCHSLCVQ 120  
Qy 121 VKDRCAPVMSAFGPPWDMLECDRFPQDNLDLCIPLASSDHLPLATEBAPKVCEACKNKND 180  
Db 121 VKDRCAPVMSAFGPPWDMLECDRFPQDNLDLCIPLASSDHLPLATEBAPKVCEACKNKND 180  
Qy 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSKTIYKLVNGVSERDLKKSVLWLK 240  
Db 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSKTIYKLVNGVSERDLKKSVLWLK 240  
Qy 241 DSIQCTCEMNDINAPYLVWGKOGGELVITSVKRWKQOGREFKRIKSLKQOC 295  
Db 241 DSIQCTCEMNDINAPYLVWGKOGGELVITSVKRWKQOGREFKRIKSLKQOC 295

#### RESULT 10

US-09-999-832A-415

; Sequence 415, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 9; Length 295;

Best Local Similarity 99.7%; Pred. No. 4.4e-133;

Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLOQPGSLLLLFLASHCCGSGARGLFLGQPDPSYKRSNCKRPANLQCHGIEYQNNRL 60  
DB 1 MLOQPGSLLLLFLASHCCGSGARGLFLGQPDPSYKRSNCKRPANLQCHGIEYQNNRL 60  
QY 61 PNLGHETMKEVLEQAGAWIPLVKMQCHPDTKKFLCSLFAFVCLDDDLDTTQPCHSLCVQ 120  
DB 61 PNLGHETMKEVLEQAGAWIPLVKMQCHPDTKKFLCSLFAFVCLDDDLDTTQPCHSLCVQ 120  
QY 121 VKRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPLPATEAPKVCACKKNND 180  
DB 121 VKRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPLPATEAPKVCACKKNND 180  
QY 181 DDNDIMETLCKNDFALKVKXEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDFALKVKXEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240  
QY 241 DLSQCTCEMNDINAPYLVMOGQGGELVITSVKRWQKGQREFKRSIRKLQC 295  
DB 241 DLSQCTCEMNDINAPYLVMOGQGGELVITSVKRWQKGQREFKRSIRKLQC 295

RESULT 11

US-09-978-189-415

; Sequence 415, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 10; Length 295;  
Best Local Similarity 99.7%; Pred. No. 4.4e-139;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLOGPGSLLLFLASHCCLGSARGLFLFGQPDFSYKGSNCKPIPANLQCHGIEYQNMRL 60  
Db 1 MLOGPGSLLLFLASHCCLGSARGLFLFGQPDFSYKGSNCKPIPVNLQCHGIEYQNMRL 60  
Qy 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCVQ 120  
Db 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCVQ 120  
Qy 121 VKDRCAPWSAFGFFWPDMLCEDRPPQDNDLCIPLASDHLLPATEEAPKVCACKNKND 180  
Db 121 VKDRCAPWSAFGFFWPDMLCEDRPPQDNDLCIPLASDHLLPATEEAPKVCACKNKND 180  
Qy 181 DDNDIMETLCNDPALKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLK 240  
Db 181 DDNDIMETLCNDPALKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLK 240  
Qy 241 DSOQCTCEEMNDINAPYLVMOQKOGGELVITSVKRWQKQREFKRISIRKLOC 295  
Db 241 DSOQCTCEEMNDINAPYLVMOQKOGGELVITSVKRWQKQREFKRISIRKLOC 295

RESULT 12  
US-09-978-608A-415  
; Sequence 415, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-415

Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLOQPGSLLLLFLASHCHCLGSARGLFLFGQDPDFSYKRSNCKPPIPANLQCHGIEYQNRL 60
Db 1 MLOQPGSLLLLFLASHCHCLGSARGLFLFGQDPDFSYKRSNCKPPIPVNLQCHGIEYQNRL 60
Qy 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
Qy 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNLDLCIPLASSDHLHPATEAPKVCACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNLDLCIPLASSDHLHPATEAPKVCACKNKND 180
Qy 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVGVSERDLKKSVLWLK 240
Db 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVGVSERDLKKSVLWLK 240
Qy 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRIISRIRKLQOC 295
Db 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRIISRIRKLQOC 295
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RESULT 13
US-09-978-585A-415
; Sequence 415, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
```

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-415

Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLOQPGSLLLLFLASHCHCLGSARGLFLFGQDPDFSYKRSNCKPPIPANLQCHGIEYQNRL 60
Db 1 MLOQPGSLLLLFLASHCHCLGSARGLFLFGQDPDFSYKRSNCKPPIPVNLQCHGIEYQNRL 60
Qy 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
Qy 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNLDLCIPLASSDHLHPATEAPKVCACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNLDLCIPLASSDHLHPATEAPKVCACKNKND 180
Qy 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVGVSERDLKKSVLWLK 240
Db 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVGVSERDLKKSVLWLK 240
Qy 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRIISRIRKLQOC 295
Db 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRIISRIRKLQOC 295
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RESULT 14
US-09-978-191A-415
; Sequence 415, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```



APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978,191A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQPGSLLLFLASHCCLSGARGFLFGQPDFSYKRNCKRPIPANLQLCHGIEYQNNRL 60
DB 1 MLQPGSLLLFLASHCCLSGARGFLFGQPDFSYKRNCKRPIPNLQLCHGIEYQNNRL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKTKFLCSLFAPVCLDDLDLDTIOPCHSLCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKTKFLCSLFAPVCLDDLDLDTIOPCHSLCVQ 120

QY 121 VKDRCAPVMSARFPWDMLECDRFPQNDLCIPLASSDHLPLPATEAPKVCCEAKNKND 180
DB 121 VKDRCAPVMSARFPWDMLECDRFPQNDLCIPLASSDHLPLPATEAPKVCCEAKNKND 180

QY 181 DNDIMETLCKNDPALKVKVEITYINRDTKILLETKSTIYKLVNGVSERDLKKSVLWLK 240
DB 181 DNDIMETLCKNDPALKVKVEITYINRDTKILLETKSTIYKLVNGVSERDLKKSVLWLK 240

QY 241 DLSQCTCEMNDINAPYLMVGKQGGELVITSVKRWQKQREFKRSIRSLKQC 295
DB 241 DLSQCTCEMNDINAPYLMVGKQGGELVITSVKRWQKQREFKRSIRSLKQC 295
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RESULT 15
US-09-978-403A-415
; Sequence 415, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 10; Length 295;

Best Local Similarity 99.7%; Pred. No. 4.4e-139;

Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLOGPGSILLFLASHCCLGARGCLFLFGOPDPSYKSNCKPIPANLQCHGIEYQNMRL 60

Db 1 MLOGPGSILLFLASHCCLGARGCLFLFGOPDPSYKSNCKPIPVNLQCHGIEYQNMRL 60

Qy 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETTQPCHSLCVQ 120

Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETTQPCHSLCVQ 120

Qy 121 VKORCAPVMSAFGPPWDMLECDRFPQDNLDLCIPLASDHLLLPATEBAPKVCEACKNKND 180

Db 121 VKORCAPVMSAFGPPWDMLECDRFPQDNLDLCIPLASDHLLLPATEBAPKVCEACKNKND 180

Qy 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVNGYSEKDLKKSVLWLK 240

Db 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSTKTIYKLVNGYSEKDLKKSVLWLK 240

Qy 241 DSLQCTCEMNDINAPYLVMGQKGGBELVITSVKRWQKGQREFKRIKRSIRKLQ 295

Db 241 DSLQCTCEMNDINAPYLVWGQKGGELVITSVKRWQKQREFKXISIRKLQC 295

Search completed: September 1, 2005, 11:13:50  
Job time : 116.895 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 10:25:34 ; Search time 31.5702 Seconds  
(without alignments)  
697.540 Million cell updates/sec

Title: US-08-949-904A-2

Perfect score: 1594

Sequence: 1 MLQFGSLLLFLASHCLLG.....WKGQREFKRISRIRKLQC 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1586	99.5	295	4	US-09-148-545-179 Sequence 179, App
2	1586	99.5	296	4	US-09-148-545-237 Sequence 237, App
3	1557	97.7	295	4	US-08-937-067-2 Sequence 2, Appli
4	1140	71.5	212	4	US-08-937-067-4 Sequence 4, Appli
5	614.5	38.6	305	4	US-09-949-016-7706 Sequence 7706, Ap
6	614.5	38.6	317	4	US-08-937-067-6 Sequence 6, Appli
7	614.5	38.6	317	4	US-09-949-016-6300 Sequence 6300, Ap
8	606	38.0	313	4	US-09-546-043-3 Sequence 3, Appli
9	606	38.0	338	4	US-09-546-043-4 Sequence 4, Appli
10	604	37.9	313	4	US-09-514-885-1 Sequence 1, Appli
11	604	37.9	313	4	US-09-949-016-6299 Sequence 6299, Ap
12	602	37.8	314	4	US-08-937-067-7 Sequence 7, Appli
13	590	37.0	113	4	US-09-087-031E-24 Sequence 24, Appl
14	585	36.7	313	4	US-09-087-031E-4 Sequence 4, Appli
15	583.5	36.6	314	4	US-09-087-031E-3 Sequence 3, Appli
16	488	30.6	295	3	US-08-893-6548-6 Sequence 6, Appli
17	478	30.0	267	4	US-09-546-043-7 Sequence 7, Appli
18	459.5	28.8	246	4	US-09-546-043-6 Sequence 6, Appli
19	433.5	27.2	280	3	US-08-893-6548-4 Sequence 4, Appli
20	407	25.5	281	3	US-08-893-6548-2 Sequence 2, Appli
21	382	24.0	195	4	US-09-546-043-5 Sequence 5, Appli
22	353	22.1	109	4	US-09-087-031E-19 Sequence 19, Appl
23	275.5	17.3	572	4	US-08-937-067-13 Sequence 13, Appl
24	275	17.3	685	4	US-08-937-067-14 Sequence 14, Appl
25	270.5	17.0	585	4	US-08-937-067-9 Sequence 9, Appli
26	267.5	16.8	537	4	US-08-937-067-11 Sequence 11, Appl
27	263.5	16.5	323	3	US-08-878-474-7 Sequence 7, Appli

Sequence 8, Appli  
Sequence 15, Appli  
Sequence 9, Appli  
Sequence 479, App  
Sequence 7544, Ap  
Sequence 3, Appli  
Sequence 3894, Ap  
Sequence 20, Appl  
Sequence 10, Appl  
Sequence 8, Appli  
Sequence 21, Appl  
Sequence 12, Appl  
Sequence 20, Appl  
Sequence 17, Appl  
Sequence 14, Appl  
Sequence 2, Appli  
Sequence 9, Appli  
Sequence 10, Appli

28 262 16.4 565 4 US-08-937-067-8  
29 260.5 16.3 114 4 US-09-087-031E-15  
30 259.5 16.3 325 3 US-08-878-474-9  
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32 259.5 16.3 371 4 US-09-949-016-7544  
33 256.5 16.1 318 3 US-08-878-474-3  
34 251 15.7 55 4 US-09-621-976-3894  
35 244.5 15.3 114 4 US-09-087-031E-20  
36 241 15.1 115 4 US-09-087-031E-10  
37 238 14.9 229 4 US-09-546-043-8  
38 237 14.9 114 4 US-09-087-031E-21  
39 235 14.7 114 4 US-09-087-031E-12  
40 231 14.5 102 4 US-09-959-392-20  
41 229.5 14.4 112 4 US-09-087-031E-17  
42 228 14.3 111 4 US-09-087-031E-14  
43 227.5 14.3 1042 4 US-09-959-392-2  
44 227 14.2 111 4 US-09-087-031E-9  
45 222.5 14.0 666 4 US-08-937-067-10

ALIGNMENTS

RESULT 1  
US-09-148-545-179  
; Sequence 179, Application US/09148545  
; Patent No. 6590075  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 76 Human Secreted Proteins  
; FILE REFERENCE: P2001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: PCT/US98/04482  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,161  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 295

Query Match          99.5%; Score 1586; DB 4; Length 295;
Best Local Similarity 99.3%; Pred. No. 7.8e-166;
Matches 293; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLOGPSLLLLFLASHCCCLGSARGLFLFGQPPFSYKRSNCKIPANLQLCHGIEYQNMRL 60
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QY 61 PNLGLHETWKEVLEQAGAWIPLVMKQCHPDPTKKFLCSLFPVCLDDLDDETIOFCHSLCVQ 120
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QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLPLPATEEAPKVCEACKNKND 180
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Db 121 VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLPLPATEEAPKVCEACKNKND 180
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QY 181 DDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
   |||||
Db 181 DDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
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QY 241 DSILOCTCEBMDINAPYLVMGOKGGELVITSVKRWQKQRFKRISIRKLQC 295
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Db 241 DSILOCTCEBMDINAPYLVMGOKGGELVITSVKRWQKQRFKRISIRKLQC 295
   |||||

RESULT 2
US-09-148-545-237
; Sequence 237, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-09-04
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
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; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-2

Query Match          97.7%; Score 1557; DB 4; Length 295;
Best Local Similarity 97.6%; Pred. No. 1.2e-162;
Matches 288; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
Db :|||||
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIQPCHSVCV 120
Db :|||||
QY 121 VKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPPATEEAPKVCCEACKNND 180
Db :|||||
QY 181 DNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKXSVLWK 240
Db :|||||
QY 241 DLSQCTCEEMNDINAPYLVMGKQGGELVITSVKRWKQGRFKRISIRKLQC 295
Db :|||||

RESULT 4
US-08-937-067-4
; Sequence 4, Application US/08937067
; Patent No. 643155
; GENERAL INFORMATION:
; APPLICANT: Unanaky, Samuil
; APPLICANT: Melkonian, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-4

Query Match          71.5%; Score 1140; DB 4; Length 212;
Best Local Similarity 99.5%; Pred. No. 5.4e-117;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
Db 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIQPCHSVCV 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIQPCHSVCV 120
QY 121 VKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPPATEEAPKVCCEACKNND 180
Db 121 VKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPPATEEAPKVCCEACKNND 180
QY 181 DNDIMETLCKNDFALKIKVKEITYINR 208
Db 181 DNDIMETLCKNDFALKIKVKEITYINR 208

RESULT 5
US-09-949-016-7706
; Sequence 7706, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7706
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7706

Query Match          38.6%; Score 614.5; DB 4; Length 305;
Best Local Similarity 43.9%; Pred. No. 5.9e-59;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 7 SLLLLFLASHCCCLGSARGLFLFG-QPDFSYKRSNCKP-----IPANLQCHGIEYQNRL 60
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QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIQPCHSVCV 120
Db 62 PNLLHESLAEVKKQASSWLPPLAKRCHSDTQVFLCSLFAFVC---LDRPIYPCRSLCEA 118
QY 121 VKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPPATEEAP---KVCEACKN 177
Db 119 VRAGCAPLMEAYGFPWPMLECHPFLDNDLCIAVQFGH--LPAT--APPVTKICAQCEM 174
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Db 175 EHSADG-LMEQMCSSDFVVKWRIKEIKENGDRKLIQAQKKKLLKPGPLKPKTKRLVL 233
QY 238 WLKDSLOCTCEEMNDINAPYLVMGKQGGELVITSVKRWKQGRFKRISIRKLQC 284
Db 234 HMKNGAGCPCPQLDSLGLAGSVLMGKVDGQLLLMAVYRWDKKMKEMK 280
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RESULT 6
US-08-937-067-6
; Sequence 6, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-6

Query Match 38.6%; Score 614.5; DB 4; Length 317;
Best Local Similarity 43.9%; Pred. No. 6.2e-59;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 7 SLLLLFLASHCCGSLGARGFLFG-QPDFSYKRSNCKP-----IPANLQCHGIEYQNRL 60
Db 14 ALALLGALHWAPARCEEYDYGWQAEPHLGHSYSKPPQCCLDIPADLPCHTVGYKMRLL 73

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCVQ 120
Db 74 PNLLHESLAEVKQQAASSWLPFLAKRCHSDTVFLCSLPAPVC---LDRPIYPCRSLSCEA 130

QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLLPATEAP---KVCEACKN 177
Db 131 VRAGCAPLMEAYGFPWPEMLHCHKFPDLNDLCIAVQFGH--LPAT--APPVTKICAQCEM 186

QY 178 KNDDNDIMETLCKNDPALKIKVKEITYINRDTKILLETKSTIYKLVNGVSRDLKKSVL 237
Db 187 EHSADG-LMEQMCSSDFVVMRIKEIKIENGDRKLIQAQKKKLLKPGPLKRRKDTKRLVL 245

QY 238 WLKDSLOQTCCEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFK 284
Db 246 HMKNGAGCPCPQLDSLGSFLVMGRKVDGQLLMAVYRWKCKKEMK 292

RESULT 7
US-08-949-016-6300
; Sequence 6300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6300
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6300

Query Match 38.0%; Score 606; DB 4; Length 313;
Best Local Similarity 41.6%; Pred. No. 5.2e-58;
Matches 124; Conservative 54; Mismatches 104; Indels 16; Gaps 6;

QY 6 GSLLLLFLASHCCGSLGARGFLFCQPD-----FSYKRSNCKPIPANLQCHGIEYQN 57
Db 16 GVLLALGGASGRGLGSEYDVVSF-QSDTGPYQSGRFYTKPPQCVDIPADLRLCHNVGYKK 74
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QY 58 MRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCCLPAPVCLDLDLDTIOPCHSL 117  
Db 75 MVLNLLHETMAEVKQQAASSVPLLNKNCHAGTQVFLCCLPAPVC---LDRPIYPCRWL 131  
QY 118 CVQVKDRCAPVMSAFGFWPMDLECDRFPQDNDLCIPLASSDHLPLATEAPKVCACKN 177  
Db 132 CEAVRDSCEPVNQFFGFWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGTTCPPCDN 190  
QY 178 KNDDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVL 237  
Db 191 ELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKDLKLV 247  
QY 238 WLKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIRKLOQ 295  
Db 248 YLKNAGADCPCHQDNLNLSHFLIMGRKVKSYLLTAIHKWDKKNKBFQKFMKKNHEC 305

RESULT 9  
US-09-546-043-4  
; Sequence 4, Application US/09546043  
; Patent No. 6600018  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffery et al.,  
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 53990  
; CURRENT APPLICATION NUMBER: US/09/546,043  
; CURRENT FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-546-043-4

Query Match 38.0%; Score 606; DB 4; Length 338;  
Best Local Similarity 41.6%; Pred. No. 5.9e-58;  
Matches 124; Conservative 54; Mismatches 104; Indels 16; Gaps 6;  
QY 6 GSLLLFLASHCCLSARGFLFGQPD-----FSYKRSNCKDIPANLQICHIEYQN 57  
Db 16 GVLLALGASGRGLSGSEYDVSF-QSDIGPYQSGRFYTKPPQCVDPADLRLCHNVGKK 74  
QY 58 MRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCCLPAPVCLDLDLDTIOPCHSL 117  
Db 75 MVLNLLHETMAEVKQQAASSVPLLNKNCHAGTQVFLCCLPAPVC---LDRPIYPCRWL 131  
QY 118 CVQVKDRCAPVMSAFGFWPMDLECDRFPQDNDLCIPLASSDHLPLATEAPKVCACKN 177  
Db 132 CEAVRDSCEPVNQFFGFWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGTTCPPCDN 190  
QY 178 KNDDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVL 237  
Db 191 ELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKDLKLV 247  
QY 238 WLKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIRKLOQ 295  
Db 248 YLKNAGADCPCHQDNLNLSHFLIMGRKVKSYLLTAIHKWDKKNKBFQKFMKKNHEC 305

RESULT 10  
US-09-514-885-1  
; Sequence 1, Application US/09514885  
; Patent No. 6656461  
; GENERAL INFORMATION:  
; APPLICANT: Imai, Kazuishi  
; APPLICANT: D'Armiento, Jeanine  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE  
; TITLE OF INVENTION: PULMONARY DISEASE  
; FILE REFERENCE: 58483.app  
; CURRENT APPLICATION NUMBER: US/09/514,885  
; CURRENT FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Human  
US-09-514-885-1

Query Match 37.9%; Score 604; DB 4; Length 313;  
Best Local Similarity 39.8%; Pred. No. 8.7e-58;  
Matches 121; Conservative 60; Mismatches 103; Indels 20; Gaps 6;  
QY 3 QGPGSLLLLFLASHCCLSARG-----GLFLFQPDFFSYKRSNCKDIPANLQICH 51  
Db 11 RGALGVLLALGAALLAVGSASEYDVSFQSDIGPYQSGR--FYTKPPQCVDPADLRLCH 68  
QY 52 GIEYQNMLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCCLPAPVCLDLDLDTI 111  
Db 69 NVGYKQVLPNLLHETMAEVKQQAASSVPLLNKNCHAGTQVFLCCLPAPVC---LDRPI 125  
QY 112 QPCHSLCVQVKDRCAPVMSAFGFWPMDLECDRFPQDNDLCIPLASSDHLPLATEAPKV 171  
Db 126 YPCRWLCEAVRDSCEPVNQFFGFWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGTTV 184  
QY 172 CEACKNKNDDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVGVSERD 231  
Db 185 CPDCNELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKD 241  
QY 232 LKKSVMKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIR 291  
Db 242 LKGLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVKSYLLTAIHKWDKKNKBFQKFMKKN 301  
QY 292 KLOQ 295  
Db 302 NHEC 305

RESULT 11  
US-09-949-016-6299  
; Sequence 6299, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6299  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6299

Query Match 37.9%; Score 604; DB 4; Length 313;  
Best Local Similarity 39.8%; Pred. No. 8.7e-58;  
Matches 121; Conservative 60; Mismatches 103; Indels 20; Gaps 6;  
QY 3 QGPGSLLLLFLASHCCLSARG-----GLFLFQPDFFSYKRSNCKDIPANLQICH 51  
Db 11 RGALGVLLALGAALLAVGSASEYDVSFQSDIGPYQSGR--FYTKPPQCVDPADLRLCH 68  
QY 52 GIEYQNMLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCCLPAPVCLDLDLDTI 111  
Db 69 NVGYKQVLPNLLHETMAEVKQQAASSVPLLNKNCHAGTQVFLCCLPAPVC---LDRPI 125

QY 112 QPCHSLCVOVKDCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLPLATEAPKV 171  
Db 126 YFCRWLCEAVRSCFVPMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPGQGTTV 184  
QY 172 CBACRKNKDDNDIMETLCKNDPALKIKVKEITYINRDTKILLETKSKTIYKLVGVSERD 231  
Db 185 CFPDNLKSE-AIIHLCASEFALRMKIKEVKKENGDKKIV--PKKKKPLKLGPIKKKD 241  
QY 232 LKXSVLWLKDSLOCTCEEMNDINAPYLVMOQOGGELVITSVKRWKOGOREFKRISRSIR 291  
Db 242 LKXLVLKNGADCPCHQDNLNLSHHFLINGRKVKSYLLTAIHKWDKKNKEFKNFMKKMK 301  
QY 292 KLOC 295  
Db 302 NHEC 305  
RESULT 12  
US-08-937-067-7  
; Sequence 7, Application US/08937067  
; Patent No. 6433155  
; GENERAL INFORMATION:  
; APPLICANT: Umansky, Samuil  
; APPLICANT: Melkonyan, Hovsep  
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING  
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/937,067  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20018.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-937-067-7  
Query Match 37.8%; Score 602; DB 4; Length 314;  
Best Local Similarity 40.1%; Pred. No. 1.5e-57;  
Matches 120; Conservative 59; Mismatches 100; Indels 20; Gaps 6;  
QY 8 LLLLFLASHCCLGASAR-----GLFLFGQPDFSYKRSNCKPAPANLQCHGIEYQ 56  
Db 17 VLLALGAALLAVGASEYDYVSFQSDIGFYQSGR--FVTKPPQCVDIPADRLCHNVGYK 74  
QY 57 NWRLNLGHETMKVLSQAGAWIPLVMKQCHPDTKKELCSLFAFPVCLDDDETQPCHS 116  
Db 75 KXVPLNLEHETMAEVKQAGSWVPLLNKNCHAGTQVFLCSLFAFVC---LDRPIYPCRW 131  
QY 117 LCVQVKDCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLPLATEAPKVCACK 176

Db 132 LCEAVRSCFVPMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNTEASKPGQGTTVCPFD 190  
QY 177 NKNDNDNDIMETLCKNDPALKIKVKEITYINRDTKILLETKSKTIYKLVGVSERDLKXSV 236  
Db 191 NELKSE-AIIHLCASEFALRMKIKEVKKENGDKKIV--PKKKKPLKLGPIKKKDLKLV 247  
QY 237 LWLKDSLOCTCEEMNDINAPYLVMOQOGGELVITSVKRWKOGOREFKRISRSIRKLOC 295  
Db 248 LYLKNGADCPCHQDNLNLSHHFLINGRKVKSYLLTAIHKWDKKNKEFKNFMKKMKNHSC 306  
RESULT 13  
US-09-087-031E-24  
; Sequence 24, Application US/09087031E  
; Patent No. 6479255  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffrey S.  
; APPLICANT: Finch, Paul  
; APPLICANT: Aaronson, Stuart  
; APPLICANT: He, Xi  
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM  
; FILE REFERENCE: 11613.13USII  
; CURRENT APPLICATION NUMBER: US/09/087,031E  
; CURRENT FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 09/087,031  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 60/050,417  
; PRIOR FILING DATE: 1997-06-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 24  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-087-031E-24  
Query Match 37.0%; Score 590; DB 4; Length 113;  
Best Local Similarity 92.9%; Pred. No. 6.5e-57;  
Matches 105; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 40 CKPIPANLQCHGIEYQNMRLPNLLGHETMKVELEQAGAWIPLVMKQCHPDTKKFLCSLF 99  
Db 1 CKPIPANLGLCHGIEYGNMRLPNLLGHETMKVELEGAGAWIPLVMKQCHPDTKKFLCSLF 60  
QY 100 APVCLDDDETQPCHSCLVQVKDCAPVMSAFGFPWPDMLCEDRFPQDNDLC 152  
Db 61 APVCLDDDETQPCHSCLVQVKDCAPVMSAFGFPWPDMLCEDRFPQDNDLC 113  
RESULT 14  
US-09-087-031E-4  
; Sequence 4, Application US/09087031E  
; Patent No. 6479255  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffrey S.  
; APPLICANT: Finch, Paul  
; APPLICANT: Aaronson, Stuart  
; APPLICANT: He, Xi  
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM  
; FILE REFERENCE: 11613.13USII  
; CURRENT APPLICATION NUMBER: US/09/087,031E  
; CURRENT FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 09/087,031  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 60/050,417  
; PRIOR FILING DATE: 1997-06-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-087-031E-4

Query Match 36.7%; Score 585; DB 4; Length 313;  
Best Local Similarity 40.1%; Pred. No. 1.1e-55;  
Matches 123; Conservative 53; Mismatches 105; Indels 26; Gaps 7;  
QY 3 QCGSLLLLFLASHCCLGSA-----RGULFGQDPDFSYKRSNCKPIPANLQCHGI 53  
DB 11 RGALGVLLALGAALLAVGASAYDYVSGSDIGPYGSGRFYTKPPGCVDPADLRLCHNV 70  
QY 54 EYQNRRLNLLGHETMKEVLEOAGAWIPLVMKQCHPDYTKKFLCSLPAPVCLDDLDDETQP 113  
DB 71 GYKKWVLPNLLSHETMAEVKGASSWVPLLNKNCHAGTGVLCSLPAPVC---LDRPIYP 127  
QY 114 CHSLCVQKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPLPATEAPK--- 170  
DB 128 CHWLCEAVRDSCEPVWGFYWPMLKCDKEP-EGDVCIAMTP-----PNATEASKPGG 181  
QY 171 --VCBCKNKNDDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGS 228  
DB 182 TTVCPCCONELKSE-AIIHLCASEFALRMKIKVKKENGDKKIV--PKKKKPLKLGPIK 238  
QY 229 ERDLKSVLWLKDSLOCTCEEEMNDINAPYLVMQKQGGELVITSVKRWKQKOREFKRISR 288  
DB 239 KDLKLLVLYLKNAGADCPCHGLDNLSHHFLINGRKVKSGYLLTAHKWDKKNKEFKNFMK 298  
QY 289 SIRKLQC 295  
DB 299 KKNHEC 305

RESULT 15

US-09-087-031E-3  
; Sequence 3, Application US/09087031E  
; Patent No. 6479255  
; GENERAL INFORMATION:  
; APPLICANT: Rubin, Jeffrey S.  
; APPLICANT: Finch, Paul  
; APPLICANT: Aaronson, Stuart  
; APPLICANT: He, Xi  
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM  
; FILE REFERENCE: 11613.13US11  
; CURRENT APPLICATION NUMBER: US/09/087,031E  
; CURRENT FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 09/087,031  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 60/050,417  
; PRIOR FILING DATE: 1997-06-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 314  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-087-031E-3

Query Match 36.6%; Score 583.5; DB 4; Length 314;  
Best Local Similarity 42.5%; Pred. No. 1.6e-55;  
Matches 116; Conservative 48; Mismatches 92; Indels 17; Gaps 6;  
QY 28 FQGPDFSYSKRSCKPIPANLQCHGIYQNMRLPNLLGHETMKEVLEOAGAWIPLVMKQC 87  
DB 46 YGSGRFYTKPPGCVDPADLRLCHNVGYKKWVLPNLLHETMAEVKGASSWVPLLNKNC 105  
QY 88 HPDTKKFLCSLPAPVCLDDLDDETIOFCHSLCVQKDRCAPVMSAFGFPWPMLECDRPPQ 147  
DB 106 HAGTGVFLCSLPAPVC---LDRPIYPCWLCEAVRDSCEPVWGFYWPMLKCDKEP- 161  
QY 148 DNDLCIPLASSDHLPLPATEAPK-----VCEACKKNKDDNDIMETLCKNDDEALIKVE 202  
DB 162 EGDVCIAMTP-----PNATEASKPGGTTCPPCDNELKSE-AIIHLCASEFALRMKIKE 215  
QY 203 ITYINRDTKIILETKSKTIYKLVGSERDLKSVLWLKDSLOCTCEEEMNDINAPYLVMQ 262

Db 216 VKKENGDKKIV--PKKKKPLKLGPIKKKDLKKLVLYLKNAGADCPCHGLDNLSHHFLINGR 273  
QY 263 KOGGELVITSVKRWKQKOREFKRISRSIRKLQC 295  
Db 274 KVKSGYLLTAHKWDKKNKEFKNFMKKNHEC 306  
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Job time : 32.5702 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 09:41:17 ; Search time 120.588 Seconds  
(without alignments)  
946.152 Million cell updates/sec

Title: US-08-949-904A-2  
Perfect score: 1594  
Sequence: 1 MLQCPGSLLLFLASHCLG.....WQKGQREPKRISIRKLQC 295

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1594	100.0	295	2 AAW49082	AAW49082 Homo sapi
3	1594	100.0	295	2 AAY06923	AAY06923 Human sec
4	1594	100.0	295	5 ABG31499	ABG31499 Human sec
5	1594	100.0	295	6 ABUS5508	ABUS5508 Human pro
6	1594	100.0	295	6 AAE34062	AAE34062 SARP 2 pr
7	1594	100.0	295	6 ABR47455	ABR47455 Breast ca
8	1594	100.0	295	7 ADF77693	ADF77693 Human ful
9	1594	100.0	295	7 ADN40027	ADN40027 Cancer/an
10	1594	100.0	295	8 ADN05090	ADN05090 Antipsori
11	1594	100.0	295	8 ADR46694	ADR46694 Cancer-as
12	1590	99.7	295	2 AAY411748	AAY411748 Human PRO
13	1590	99.7	295	3 AAB44304	AAB44304 Human PRO
14	1590	99.7	295	5 ABB84861	ABB84861 Human PRO
15	1590	99.7	295	5 ABB95467	ABB95467 Human ang
16	1590	99.7	295	6 ABO25250	ABO25250 Novel hum
17	1590	99.7	295	6 ABU72256	ABU72256 Novel hum
18	1590	99.7	295	6 ABU84936	ABU84936 Human sec
19	1590	99.7	295	6 ABU61134	ABU61134 Human PRO
20	1590	99.7	295	6 ABU80403	ABU80403 Human sec
21	1590	99.7	295	6 ADA24954	ADA24954 Novel hum
22	1590	99.7	295	6 ABO19705	ABO19705 Novel hum
23	1590	99.7	295	6 ADA12615	ADA12615 Human sec
24	1590	99.7	295	6 ABO19596	ABO19596 Novel hum
25	1590	99.7	295	7 ADB73921	ADB73921 Human PRO

ALIGNMENTS

RESULT 1  
AAW82588  
ID AAW82588 standard; propein; 295 AA.  
XX AC AAW82588;  
XX DT 01-MAR-1999 (first entry)  
XX DE Human ATG-1622 protein.

XX ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;  
KW diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;  
KW heart disease; hypertension; kidney diseases; insulin resistance;  
KW lipodystrophy; diabetes; central nervous system; CNS; gene mapping;  
KW linkage analysis.  
XX OS Homo sapiens.  
XX PN EP879887-A1.  
XX PD 25-NOV-1998.  
XX PF 14-MAY-1998; 98EP-00303809.  
XX PR 21-MAY-1997; 97US-0047251P.  
XX PA 13-JUN-1997; 97US-00874156.  
XX PI (SMIK) SMITHKLINE BEECHAM CORP.  
XX PT Hu E, Zhu Y;  
XX PS WPI; 1998-596879/51.  
XX PS N-PSDB; AAV69384.  
XX PT New human secreted protein ATG-1622 polypeptide and polynucleotide -  
XX PS useful as diagnostic reagents and for prevention and treatment of Central  
XX PS Nervous System diseases and diabetes.  
XX PS Claim 11; Page 22-23; 28pp; English.  
XX PS This sequence represents the human ATG-1622 protein which is related to  
XX PS murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for  
XX PS diagnosing susceptibility to diseases by detecting mutations in the ATG-  
XX PS 1622 gene and can diagnose diseases associated with ATG-1622 imbalance.  
XX PS The polypeptides can be used to screen for agonists and antagonists which  
XX PS can be used in treatment to activate or inhibit ATG-1622 activity. The  
XX PS ATG-1622 polypeptide can be administered directly or as a vaccine to

AdB76637 Human PRO  
AdC44063 Human sec  
AdC61823 Human sec  
AdC63787 Human sec  
AdC66887 Human sec  
AdC69011 Human sec  
AdC63071 Human sec  
AdC68136 Human sec  
AdC41456 Human sec  
AdC67511 Human sec  
AdC62447 Human sec  
AdC42080 Human sec  
AdD10379 Human sec  
AdD11339 Human sec  
AdD37132 Human sec  
AdE49449 Human sec  
AdE35503 Human sec  
AdE16617 Human sec  
AdD73232 Human sec  
AdD72590 Human sec

CC inoculate against disease. Diseases which can be diagnosed, prevented or treated by the ATG-1622 polypeptide or polynucleotides include heart disease, hypertension, kidney diseases, obesity, insulin resistance, CC lipodystrophy, diabetes and central nervous system (CNS) diseases. The CC ATG-1622 polypeptide is also useful for mapping the gene to a chromosome, CC allowing gene inheritance to be studied through linkage analysis

XX Sequence 295 AA;

SQ Query Match 100.0%; Score 1594; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCLSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
DB 1 MLQPGSLLLLFLASHCCLSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPAPVCLDDLETIQPCHSLCVQ 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPAPVCLDDLETIQPCHSLCVQ 120  
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPPATEAPKVCEACKNKND 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPPATEAPKVCEACKNKND 180  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240  
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240  
QY 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRSIRKLQC 295  
DB 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRSIRKLQC 295

RESULT 2

AAW49082  
ID AAW49082 standard; protein; 295 AA.

XX AC AAW49082;

DT 09-NOV-1998 (first entry)

XX Homo sapiens SDF-5 protein.

XX SDF-5; frazzled; osteoarthritis; rheumatoid arthritis; cell formation;  
KW proliferation; differentiation; diabetes; pancreatic cancer;  
KW wound healing; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Peptide 1..20  
/note= "signal peptide"

XX WO9835043-A1.

PD 13-AUG-1998.

XX 15-OCT-1997; 97WO-US018369.

PR 06-FEB-1997; 97US-00796153.

PR 08-MAY-1997; 97US-00848439.

XX (GEMY ) GENETICS INST INC.

XX Lavallie ER, Racie LA;

XX WPI: 1998-447240/38.

DR N-PSDB; AAV32930.

XX Isolated DNA encoding human SDF-5 protein - useful for controlling  
PT growth, differentiation etc. of cells, particularly of chondrocytes for  
PT treatment of arthritis etc., also pancreatic cells.

XX PS Claim 18; Page 57-58; 69pp; English.

XX The sequence is that of human SDF-5, a member of the Frazzled protein family. Cells transformed with a vector containing the sequence are used to regulate genes, particularly pancreatic genes, or in combination with bone morphogenic protein 2 (BMP2), to increase differentiation of progenitor cells into chondrocytes. The protein may be used to treat osteoarthritis, rheumatoid arthritis, or articular cartilage defects, CC also to increase/inhibit cell formation, growth, differentiation, CC proliferation and/or maintenance in many other organs or tissues, e.g. CC for prevention or treatment of pancreatic cancer, diabetes (by inducing de novo formation of islet cells), other tissue defects, also to improve CC healing of wounds and to increase survival of nervous system cells, e.g. CC in cases of transplants. The coding sequence can be used in gene therapy, CC and its fragments to detect related mRNA, while the protein is also used to generate antibodies, useful for affinity purification and as CC immunoassay reagents. Many other potential uses/activities for the gene CC and its encoded are contemplated but not exemplified, e.g. as cytokines, CC immuno-suppressants or immunostimulants, regulators of haematopoiesis, as CC fertility-control agents, haemostatic or thrombolytic agents, anti-inflammatory agents, antimicrobials, modulators of biorhythms and many CC more

XX Sequence 295 AA;

Query Match 100.0%; Score 1594; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCLSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60

DB 1 MLQPGSLLLLFLASHCCLSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPAPVCLDDLETIQPCHSLCVQ 120

DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPAPVCLDDLETIQPCHSLCVQ 120

QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPPATEAPKVCEACKNKND 180

DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPPATEAPKVCEACKNKND 180

QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240

DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240

QY 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRSIRKLQC 295

DB 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKGQREFKRSIRKLQC 295

RESULT 3

AAW06923  
ID AAW06923 standard; protein; 295 AA.

XX AC AAW06923;

XX 01-JUL-1999 (first entry)

XX Human secreted protein ligand ATG-1622 polypeptide.

XX Human; ATG-1622 polypeptide; secreted protein ligand; 7-TM receptor;  
KW frizzled family; heart disease; hypertension; kidney disease; obesity;  
KW insulin resistance; lipodystrophy; diabetes; CNS disease.

XX Homo sapiens.

XX CA2229436-A.

XX 21-NOV-1998.

XX 23-APR-1998; 98CA-02229436.



PR 21-MAY-1997; 97US-0047251P.  
PR 13-JUN-1997; 97US-00874156.  
PR 20-MAR-1998; 98US-00044885.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Hu E, Zhu Y;  
PI WPI; 1999-244679/21.  
DR N-PSDB; AAX34662.  
XX  
XX New secreted protein ligand polypeptide (ATG-1622) of 7-TM (frizzled family) receptors, useful for diagnosis, prevention and treatment of obesity, lipodystrophy, hypertension and heart disease.  
XX  
XX Claim 11; Page 10-11; 42pp; English.  
XX  
XX This represents a human ATG-1622 polypeptide, a secreted protein ligand for 7-TM (frizzled family) receptors. ATG-1622 polypeptides and CC polynucleotides are useful for diagnosing a disease or susceptibility to a disease by determining the presence/absence of a mutation in the ATG-1622 gene, and/or analysing for the presence or amount of ATG-1622 expressed in the patient. ATG-1622 expressing cells are useful for CC identifying modulators of the polypeptide which are can be used to treat CC conditions associated with a lack or excess of ATG-1622 polypeptide. CC Diseases diagnosed, prevented or treated include heart disease, CC hypertension, kidney diseases, obesity, insulin resistance, CC lipodystrophy, diabetes and CNS diseases. ATG-1622 protein may be useful CC for treating or preventing the onset of obesity. ATG-1622 polypeptides CC are also useful for mapping genes to chromosomes, allowing gene CC inheritance to be studies through linkage analysis  
XX  
XX Sequence 295 AA;  
SQ  
Query Match 100.0%; Score 1594; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MLQPGSLLLFLASHCCGLSGARGFLFGQPPFSYKRSNCKDIPANLQLCHGIEYQNRL 60  
DB 1 MLQPGSLLLFLASHCCGLSGARGFLFGQPPFSYKRSNCKDIPANLQLCHGIEYQNRL 60  
OY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTTKKFLCSLPAPVCLDLDLDTIQCHSLCQV 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTTKKFLCSLPAPVCLDLDLDTIQCHSLCQV 120  
OY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCLIPASSDHLPLPATEEAPKVCACKNKD 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCLIPASSDHLPLPATEEAPKVCACKNKD 180  
OY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMUK 240  
DB 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMUK 240  
OY 241 DLSQCTCEBMNDINAPYLVMGKQGGELVITSYKRWKQGRFKRISIRKLQC 295  
DB 241 DLSQCTCEBMNDINAPYLVMGKQGGELVITSYKRWKQGRFKRISIRKLQC 295  
RESULT 4  
ABG31499  
ID ABG31499 standard; protein; 295 AA.  
XX  
XX AC ABG31499;  
XX  
XX 09-SEP-2004 (revised)  
DT 28-NOV-2002 (first entry)  
XX  
XX Human secreted apoptosis-related protein 1 (SARP-1).  
XX  
XX Human; secreted apoptosis-related protein 1; SARP-1; scleroderma; systemic sclerosis; fibrotic disease; liver cirrhosis; keloid; interstitial pulmonary fibrosis; Dupuytren's contracture; scarring;  
KW

KW wound healing; postoperative adhesion; reactive fibrosis;  
KW chronic heart failure; myocardial infarction; inflammatory disorder;  
KW lung inflammation; idiopathic pulmonary fibrosis; systemic disease;  
KW rheumatoid arthritis; anti-sclerotic; protein therapy.  
XX  
XX Homo sapiens.  
OS Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..50  
FT /note= "Theoretical N-terminal sequence of immature SARP-1"  
FT  
FT Cleavage-site 19..20  
FT /note= "Position of 1st predicted signal cleavage"  
FT Protein 21..295  
FT /note= "Specifically claimed in Claim 2"  
FT Protein 24..295  
FT /note= "Specifically claimed in Claim 2"  
FT Cleavage-site 24..25  
FT /note= "Position of 2nd predicted signal cleavage"  
FT Protein 25..295  
FT /note= "Specifically claimed in Claim 2"  
FT Protein 26..295  
FT /note= "Specifically claimed in Claim 2"  
FT Protein 27..295  
FT /note= "Specifically claimed in Claim 2"  
FT Protein 28..295  
FT /note= "Specifically claimed in Claim 2"  
FT Cleavage-site 36..37  
FT /note= "Tryptic like cleavage"  
FT Protein 37..295  
FT /note= "Specifically claimed in Claim 2"  
XX  
XX WO200246225-A2.  
XX  
XX 13-JUN-2002.  
XX  
XX 30-NOV-2001; 2001WO-EP013992.  
XX  
XX 06-DEC-2000; 2000EP-00126771.  
XX 17-AUG-2001; 2001EP-00118888.  
XX  
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX  
XX Plater-Zyberk C, Power C, Colinge J;  
XX  
XX WPI; 2002-705807/76.  
XX N-PSDB; ABS53585.  
XX  
XX Use of human Secreted Apoptosis-Related Protein (SARP)-1 and SARP-1 nucleic acids for the treatment of sclerosis, especially systemic sclerosis.  
XX  
XX Claim 2; Fig 5; 63pp; English.  
XX  
XX The present invention relates to the use of human secreted apoptosis-related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which stimulates the release or potentiates the activity of endogenous SARP-1 for the treatment of scleroderma. The SARP-1 protein binds to and CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can CC be used in protein therapy, and the polynucleotide sequences encoding CC SARP-1 can be used in gene therapy. SARP-1 polypeptide and polynucleotide CC sequences, and pharmaceutical compositions comprising SARP-1 are useful CC for the treatment of scleroderma, especially systemic sclerosis. They may CC also be used to treat fibrotic diseases (e.g. liver cirrhosis, CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and CC other scarring/wound healing abnormalities, postoperative adhesions and CC reactive fibrosis), chronic heart failure (particularly after myocardial CC infarction), disorders involving inflammation of the lung (e.g. CC idiopathic pulmonary fibrosis), and systemic diseases (e.g. rheumatoid CC arthritis). The present sequence represents human SARP-1  
XX  
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key



DE SARP 2 protein.  
XX  
KW Drug screening; toxicology assay; signalling pathway; SARP 2.  
XX  
OS Unidentified.  
XX  
PN WO200290992-A2.  
XX  
PD 14-NOV-2002.  
XX  
XX 29-APR-2002; 2002WO-GB001946.  
XX  
XX 04-MAY-2001; 2001GB-00011004.  
XX  
XX (AXOR-) AXORDIA LTD.  
XX  
XX Andrews P, Draper J, Walsh J;  
XX  
XX WPI; 2003-120579/11.  
DR N-PSDB; AAD52560.  
XX  
XX Identifying biologically active agents comprises cloning transfected  
PT cells into a cell array, exposing the array to an agent to be tested, and  
PT detecting signals generated by a reporter molecule as a result of  
PT exposure to the agent.  
XX  
XX Claim 16; Fig 76; 90pp; English.  
XX  
XX The present invention relates to a novel screening method which enables  
CC the identification of biologically active agents which mediate their  
CC effect through the activation of genes. The method involves providing a  
CC population of cells stably transfected with a nucleic acid encoding a  
CC reporter molecule, cloning the transfected cells into a cell array,  
CC exposing the array to at least one agent to be tested and detecting a  
CC signal generated by the reporter molecule as a result of exposure to the  
CC agent. The method is useful in identifying biologically active agents and  
CC the genes through which the agents act, in screening potential drugs for  
CC their ability to activate certain drug targets in a high-throughput  
CC assay, in identifying relationships between signalling pathways and  
CC specific signals that could be useful in eventually directing the  
CC differentiation of embryonic stem cells and in toxicology assays by  
CC testing for unwanted activation or inhibition of specific signalling  
CC pathways. The present sequence is SARP 2 protein used to illustrate the  
CC method of the invention  
XX  
XX Sequence 295 AA;  
SQ

Query Match 100.0%; Score 1594; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQGGPSLLLLFLASHCCCLGSGARGFLFGQDPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
DB 1 MLQGGPSLLLLFLASHCCCLGSGARGFLFGQDPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
QY 61 PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDDLDDETIQCHSLVCV 120  
DB 61 PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDDLDDETIQCHSLVCV 120  
QY 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVCACKNKND 180  
DB 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVCACKNKND 180  
QY 181 DNDIMETLCKNDFAIKVKETIYNRDTKIILETKSTIYKLVGVSERDLKKSVMWK 240  
DB 181 DNDIMETLCKNDFAIKVKETIYNRDTKIILETKSTIYKLVGVSERDLKKSVMWK 240  
QY 241 DSILOCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKQKQREPKRISIRKLQC 295  
DB 241 DSILOCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKQKQREPKRISIRKLQC 295

RESULT 7

ABR47455  
ID ABR47455 standard; protein; 295 AA.  
XX  
AC ABR47455;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Breast cancer associated protein sequence SEQ ID NO:142.  
XX  
KW Human; breast cancer; cytostatic; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO2003004989-A2.  
PN  
XX 16-JAN-2003.  
PD  
XX 21-JUN-2002; 2002WO-US019669.  
PF  
XX 21-JUN-2001; 2001US-0299887P.  
PR 27-JUN-2001; 2001US-0301572P.  
PR 18-JUL-2001; 2001US-0306501P.  
PR 25-SEP-2001; 2001US-0325002P.  
PR 05-MAR-2002; 2002US-0362585P.  
PR 14-MAY-2002; 2002US-0380391P.  
XX  
XX (MILL-) MILLENIUM PHARM INC.  
PA  
XX Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;  
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;  
XX  
XX WPI; 2003-210381/20.  
DR N-PSDB; ACC50147.  
XX  
XX Breast cancer diagnosis or treatment by comparing the level of expression  
PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.  
XX  
XX Claim 1; SEQ ID NO 142; 128pp; English.  
XX  
XX The present invention describes a method for assessing whether a patient  
CC is afflicted with breast cancer. The method comprises comparing the level  
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
CC ABR47386 to ABR47632) in a patient sample and the normal level of  
CC expression of the marker in a control non-breast cancer sample, where a  
CC significant increase in the level of expression of the marker in the  
CC patient sample and the normal level is an indication that the patient is  
CC afflicted with breast cancer. The breast cancer associated sequences from  
CC the present invention have cytostatic activities and can be used in gene  
CC therapy. The method is useful for diagnosing and treating breast cancer.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 295 AA;  
SQ

Query Match 100.0%; Score 1594; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQGGPSLLLLFLASHCCCLGSGARGFLFGQDPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
DB 1 MLQGGPSLLLLFLASHCCCLGSGARGFLFGQDPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
QY 61 PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDDLDDETIQCHSLVCV 120  
DB 61 PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDDLDDETIQCHSLVCV 120  
QY 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVCACKNKND 180  
DB 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVCACKNKND 180

QY 181 DDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETYSKTIYKLVGVSERDLKKSIVLWK 240  
 Db |||||  
 181 DDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETYSKTIYKLVGVSERDLKKSIVLWK 240  
 QY 241 DSIQCTCEEMNDINAPYLVMGQKQGGLVITSVKRWQKQREFFKRISIRKLQC 295  
 Db |||||  
 241 DSIQCTCEEMNDINAPYLVMGQKQGGLVITSVKRWQKQREFFKRISIRKLQC 295

## RESULT 8

ADP77693  
 ID ADF77693 standard; protein; 295 AA.  
 XX  
 AC ADF77693;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human full length Frazzled family protein SDF-5.  
 XX  
 KW Human; Frazzled family protein; SDF-5; pancreatic gene;  
 KW chondrocyte differentiation; cartilage tissue formation; tissue repair;  
 KW pancreatic tissue repair; cartilage disorders; osteoarthritis;  
 KW rheumatoid arthritis; articular cartilage defect; nutritional source;  
 KW nutritional supplement; immune deficiency; infection; HIV infection;  
 KW hepatitis; cancer; diabetes; inflammation; asthma; neurological disorder;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease.  
 XX  
 OS Homo sapiens.

## Key Location/Qualifiers

FT Peptide 1..20  
 FT Region /note="Signal peptide"  
 FT Region 18..295  
 FT Region /note="Claimed in claim 2"  
 FT Region 19..295  
 FT Region /note="Claimed in claim 2"  
 FT Region 20..295  
 FT Region /note="Claimed in claim 2"  
 FT Protein 21..295  
 FT /label="Mature SDF 5"  
 FT Region /note="Claimed in claim 2"  
 FT Region 22..295  
 FT Region /note="Claimed in claim 2"  
 FT Region 23..295  
 FT Region /note="Claimed in claim 2"  
 FT Region 24..295  
 FT Region /note="Claimed in claim 2"  
 FT Region 25..295  
 FT Region /note="Claimed in claim 2"  
 XX

US2003175855-A1.

PN 18-SEP-2003.

XX 15-OCT-1997; 97US-00949904.

XX 06-FEB-1997; 97US-00796153.

PR 08-MAY-1997; 97US-00848433.

XX (LAVA/) LAVALLIE E R.

PA (RACI/) RACIE L A.

XX Lavallie ER, Racie LA;

PI WPI; 2003-898533/82.

DR N-PSDB; ADF77692.

XX

PT New human SDF-5 DNA, useful for inducing formation, growth,  
 PT differentiation, proliferation or maintenance of chondrocytes or  
 PT cartilage tissues, or as nutritional sources or supplements.

XX Claim 18; SEQ ID NO 2; 24pp; English.

PS

CC The invention relates to an isolated DNA sequence encoding mature or full  
 CC length human SDF-5 (a frazzled family member) or its defined fragments,  
 CC or which hybridises to it under stringent hybridisation conditions and  
 CC encodes a protein that exhibits Frazzled activity. Also included are a  
 CC vector comprising the above DNA molecule in operative association with an  
 CC expression control sequence, a host cell transformed with the vector, a  
 CC method for producing purified human SDF-5 protein, a purified human SDF-5  
 CC polypeptide, a composition comprising a therapeutic amount of at least  
 CC one human SDF-5 polypeptide cited above, a method for altering the  
 CC regulation of pancreatic genes in a patient (comprising administering to  
 CC the patient an amount of the composition cited above), antibodies to a  
 CC purified human SDF-5 protein and a method for increasing the  
 CC differentiation of cells into chondrocytes, comprising applying a  
 CC composition comprising BMP-2 (Bone morphogenetic protein-2) and SDF-5.  
 CC The DNA and protein are useful in regulating the binding of Wnt (wingnut)  
 CC genes to their receptor or in inducing formation, growth,  
 CC differentiation, proliferation and/or maintenance of chondrocytes, such  
 CC cartilage tissue, and for other tissue repair, such as pancreatic tissue  
 CC repair. These may be used in the treatment of articular cartilage defects.  
 CC As osteoarthritis, rheumatoid arthritis or activity of other tissue  
 CC These may also be used for augmenting the activity of other tissue  
 CC regenerating and differentiation factors. In addition, the protein and  
 CC DNA are used as nutritional sources or supplements and in treating  
 CC various immune deficiencies and disorders (e.g. infections, HIV,  
 CC hepatitis, cancer, diabetes, inflammation or asthma) or neurological  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's  
 CC disease). The present sequence represents full length human SDF-5.  
 XX

## Sequence 295 AA;

Query Match 100.0%; Score 1594; DB 7; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 4e-150;  
 Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCGSGARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
 Db |||||  
 1 MLQPGSLLLLFLASHCCGSGARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60  
 QY 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKFLCSLFAFVCLDDLDDETTPCHSLCVQ 120  
 Db |||||  
 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDTKFLCSLFAFVCLDDLDDETTPCHSLCVQ 120  
 QY 121 VKRCAPVWSAFGPPWPDMLCEDRFPQNDLICIPLASSDHLLPATEAPKVEACKNKND 180  
 Db |||||  
 121 VKRCAPVWSAFGPPWPDMLCEDRFPQNDLICIPLASSDHLLPATEAPKVEACKNKND 180  
 QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETYSKTIYKLVGVSERDLKKSIVLWK 240  
 Db |||||  
 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETYSKTIYKLVGVSERDLKKSIVLWK 240  
 QY 241 DSIQCTCEEMNDINAPYLVMGQKQGGLVITSVKRWQKQREFFKRISIRKLQC 295  
 Db |||||  
 241 DSIQCTCEEMNDINAPYLVMGQKQGGLVITSVKRWQKQREFFKRISIRKLQC 295

## RESULT 9

ADN40027  
 ID ADN40027 standard; protein; 295 AA.

XX ADN40027;

XX 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.

XX Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
 KW vulnery; gene therapy; vaccine.  
 XX

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OS Homo sapiens.
XX WO2003042661-A2.
XX 22-MAY-2003.
XX 13-NOV-2002; 2002WO-US036810.
XX 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359777P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397773P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezl PA;
PI Mack DR, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
XX N-PSDB; ADN39810.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO C397; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX antibodies and methods are useful for diagnosing, prognosing and treating
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX neovascularisation syndromes, scarring and uterine fibroids. They may
XX also be useful in wound healing and in contraception. The present
XX sequence represents a polypeptide of the invention.
XX
XX Sequence 295 AA;
XX
XX Query Match 100.0%; Score 1594; DB 7; Length 295;
XX Best Local Similarity 100.0%; Pred. No. 4e-150;
XX Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLOQPGSLLLLFLASHCCLGARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
XX
XX 1 MLOQPGSLLLLFLASHCCLGARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
XX
XX 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
XX
XX 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
XX
XX 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLHPATEAPKVCACKNKND 180
XX
XX 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLHPATEAPKVCACKNKND 180
XX
XX 181 DDNDIMETLCKNDFALKIKVKEITYINRDTHKIILETKSKTIYKLVNGVSRDLKKSVLWLK 240
XX
XX 181 DDNDIMETLCKNDFALKIKVKEITYINRDTHKIILETKSKTIYKLVNGVSRDLKKSVLWLK 240
XX
XX 241 DSLOCTCEEMNDINAPYLVMSKQGGELVITSVKRWKQGQREPKRISIRKLCQ 295
XX
XX 241 DSLOCTCEEMNDINAPYLVMSKQGGELVITSVKRWKQGQREPKRISIRKLCQ 295
XX
XX RESULT 10
XX ADN05090
XX ID ADN05090 standard; protein; 295 AA.
XX
XX AC ADN05090;
XX
XX 01-JUL-2004 (first entry)
XX
XX Antipsoriatic protein sequence #724.
XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004028479-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030907.
XX
XX 25-SEP-2002; 2002US-0414006P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX Wu TD;
XX
XX WPI; 2004-305105/28.
XX N-PSDB; ADN05089.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
XX pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
XX
XX Claim 9; SEQ ID NO 1484; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
XX treating psoriasis or a sequence having at least 80% identity to the
XX above sequences. The nucleic acid is useful for preparing a composition
XX for diagnosing or treating psoriasis in a mammal. This sequence
XX corresponds to one of the polypeptides of the invention.
XX
XX Sequence 295 AA;
XX
XX Query Match 100.0%; Score 1594; DB 8; Length 295;
XX Best Local Similarity 100.0%; Pred. No. 4e-150;
XX Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLOQPGSLLLLFLASHCCLGARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
XX
XX 1 MLOQPGSLLLLFLASHCCLGARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60
XX
XX 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
XX
XX 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
XX
XX 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLHPATEAPKVCACKNKND 180
XX
XX 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLHPATEAPKVCACKNKND 180
```

QY 181 DDNDIMETLCKNDFAIKVKVEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDFAIKVKVEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
QY 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWKQGREFKRISIRKLOC 295  
DB 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWKQGREFKRISIRKLOC 295  
RESULT 11  
ADR46694  
ID ADR46694 standard; protein; 295 AA.  
XX  
AC ADR46694;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Cancer-associated protein, SEQ ID 107.  
XX  
KW Cytostatic; Gene Therapy; cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004073657-A2.  
XX  
PD 02-SEP-2004.  
XX  
PF 19-FEB-2004; 2004WO-US005455.  
XX  
PR 19-FEB-2003; 2003US-0448784P.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Aziz N, Gish KC, Wilson KE, Zlotnik A;  
XX  
DR WPI; 2004-652787/63.  
DR N-PSDB; ADR46636.  
XX  
PT Detecting a pathological cell in a patient for diagnosing or treating  
PT cancer by detecting in a biological sample from the patient genes whose  
PT expression are up-regulated or down-regulated in specific cancers.  
XX  
PS Claim 1; SEQ ID NO 107; 375pp; English.  
XX  
CC The present invention relates to a method for detecting cancer in a  
CC patient. The method comprises detecting in a biological sample from the  
CC patient a nucleotide or protein sequence comprising a sequence that is at  
CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or  
CC protein sequence (ADR46646-ADR46703). The method is useful for detecting  
CC cancer for preparing a composition for diagnosing or treating cancer.  
XX  
SQ Sequence 295 AA;  
Query Match 100.0%; Score 1594; DB 8; Length 295;  
Best Local Similarity 100.0%; Pred. No. 4e-150;  
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQPGSLLLLFLASHCCIGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRL 60  
DB 1 MLQPGSLLLLFLASHCCIGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRL 60  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCSHLCVQ 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCSHLCVQ 120  
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLIPATEEAPKVCCEACKNKND 180  
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLIPATEEAPKVCCEACKNKND 180  
QY 181 DDNDIMETLCKNDFAIKVKVEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDFAIKVKVEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240

QY 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWKQGREFKRISIRKLOC 295  
DB 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWKQGREFKRISIRKLOC 295  
RESULT 12  
AAAY41748  
ID AAAY41748 standard; protein; 295 AA.  
XX  
AC AAAY41748;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO697 protein sequence.  
XX  
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX  
OS Homo sapiens.  
XX  
PN WO9946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-US005028.  
XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079234P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.



PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.  
XX Claim 12; Fig 167; 636pp; English.  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytotactic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
XX Sequence 295 AA;  
SQ  
Query Match 99.7%; Score 1590; DB 3; Length 295;  
Best Local Similarity 99.7%; Pred. No. 1e-149;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLQPGSLLLLFLASHCCLGSARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNNRL 60  
Db 1 MLQPGSLLLLFLASHCCLGSARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNNRL 60  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLVCQ 120  
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLVCQ 120  
QY 121 VKDRCAPVMSARGFPWDMLECDRPPQNDLCLPIASSDHLPLATEAPKVCACNKNQD 180  
Db 121 VKDRCAPVMSARGFPWDMLECDRPPQNDLCLPIASSDHLPLATEAPKVCACNKNQD 180  
QY 181 DNDIMETLCKNDFAKIKVKEITVINRDTKILLETKSTIYKLVNGVSERDLKKSVMWLK 240  
Db 181 DNDIMETLCKNDFAKIKVKEITVINRDTKILLETKSTIYKLVNGVSERDLKKSVMWLK 240  
QY 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKQREFKRSIRKLQ 295  
Db 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKQREFKRSIRKLQ 295  
RESULT 14  
ABB84861  
ID ABB84861 standard; protein; 295 AA.  
XX AC ABB84861;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO697 protein sequence SEQ ID NO:90.  
XX KW Human; angiogenesis; cardiast; cytotactic; antiangiogenic; hypotensive;  
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX OS Homo sapiens.  
XX PN WO200200690-A2.  
XX XX  
PD 03-JAN-2002.  
XX XX  
PF 20-JUN-2001; 2001WO-US019692.  
XX PR 23-JUN-2000; 2000US-0213637P.  
PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 22-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 25-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 30-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-090516/12.  
XX N-PSDB; ABL88116.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX Claim 11; Fig 90; 565pp; English.  
XX ABL88072 to ABL88259 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention  
XX  
XX Sequence 295 AA;  
Query Match 99.7%; Score 1590; DB 5; Length 295;  
Best Local Similarity 99.7%; Pred. No. 1e-149;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLQPGSLLLLFLASHCCLGSARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNNRL 60  
Db 1 MLQPGSLLLLFLASHCCLGSARGFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNNRL 60



Qy	61	PNLLGHETNKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSLCVQ	120
Db	61	PNLLGHETNKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSLCVQ	120
Qy	121	VKDRCAPVMSAFGFPWMDLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCEACKNKND	180
Db	121	VKDRCAPVMSAFGFPWMDLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCEACKNKND	180
Qy	181	DDNDIMETLCKNDFALKIKVKEITYINRDTKIILLETSKTIYKLVGVSERDLKKSVLWLK	240
Db	181	DDNDIMETLCKNDFALKIKVKEITYINRDTKIILLETSKTIYKLVGVSERDLKKSVLWLK	240
Qy	241	DSLOQTCBEMNDINAPYLVMGKQGGELVITSVTRWKGQREFKRISRSIRKLQOC	295
Db	241	DSLOQTCBEMNDINAPYLVMGKQGGELVITSVTRWKGQREFKRISRSIRKLQOC	295
RESULT 15			
ABB95467			
ID	ABB95467 standard; protein; 295 AA.		
XX			
AC	ABB95467;		
XX			
DT	19-JUL-2002 (first entry)		
XX			
DE	Human angiogenesis related protein PRO697 SEQ ID NO: 90.		
XX			
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;		
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;		
KW	cardiac; cytotatic; antiangiogenic; hypotensive; vulnery;		
KW	antiarteriosclerotic.		
XX			
OS	Homo sapiens.		
XX			
PN	WQ200208284-A2.		
XX			
PD	31-JAN-2002.		
XX			
PF	09-JUL-2001; 2001WO-US021735.		
XX			
PR	20-JUL-2000; 2000US-0219556P.		
PR	25-JUL-2000; 2000US-0220624P.		
PR	25-JUL-2000; 2000US-0220664P.		
PR	28-JUL-2000; 2000WO-US020710.		
PR	02-AUG-2000; 2000US-0222695P.		
PR	17-AUG-2000; 2000US-00643657.		
PR	23-AUG-2000; 2000WO-US023322.		
PR	24-AUG-2000; 2000WO-US023328.		
PR	07-SEP-2000; 2000US-0230978P.		
PR	18-SEP-2000; 2000US-00664610.		
PR	18-SEP-2000; 2000US-00665350.		
PR	24-OCT-2000; 2000US-0242922P.		
PR	08-NOV-2000; 2000US-00709238.		
PR	08-NOV-2000; 2000WO-US030952.		
PR	10-NOV-2000; 2000WO-US030873.		
PR	01-DEC-2000; 2000WO-US032678.		
PR	20-DEC-2000; 2000US-00747259.		
PR	20-DEC-2000; 2000WO-US034956.		
PR	22-JAN-2001; 2001US-00776709.		
PR	28-FEB-2001; 2001US-00796498.		
PR	28-FEB-2001; 2001WO-US006520.		
PR	01-MAR-2001; 2001WO-US006666.		
PR	09-MAR-2001; 2001US-00802706.		
PR	14-MAR-2001; 2001US-00808689.		
PR	22-MAR-2001; 2001US-00816744.		
PR	05-APR-2001; 2001US-00828366.		
PR	10-MAY-2001; 2001US-00854208.		
PR	10-MAY-2001; 2001US-00854280.		
PR	25-MAY-2001; 2001US-00866028.		
PR	25-MAY-2001; 2001US-00866034.		
PR	25-MAY-2001; 2001WO-US017092.		
PR	30-MAY-2001; 2001US-00870574.		

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A;Reference number: JC7127; MUID:20012777; PMID:10544037

A;Accession: JC7127

**A;Status: preliminary**

A:Molecule type: mRNA

A; molecule type: mRNA  
A:Residues: 1-537 -KTR-

A;Rebiques: I-537 <KIR>  
A:Cross-references: INT

A; Cross-ret

C;Genetics:

A;Gene: FZD4

A;Map position: 11 region q14 - q21

**Alignment Scores:**

ATTACHMENT SCORES:  
Pred. No.: 2 096-11 Length: 537

Pred. No.:	2.09e-11	Length:	537
Score:	200 00	Weight:	73

Score:	290.00	Matches:	72
Score:	290.00	Matches:	72
Score:	290.00	Matches:	72

Percent Similarity: 45.26%  
Conservative: 33

Best Local Similarity: 31.03% Mismatches: 93

Query Match:	8.09%	Indels:	34
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US-08-949-904A-1 (1-2027) x JC7127 (1-537)

238 CCGGGTGGGGCCACGATGCTGACGGCCCTGGTGGTG-----CTGGATGCTTC 288

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238 CGGGTGGCGGCCACGATGCTGCAGGCTTCGGTGTG-----CAGCTGCTC 288

[illegible]

Db 4 ArgGlyAlaGlyProSerValProGlyAlaProGlyGlyValGlyLeuSerLeuGlyLeu 23

Qy 289 TTCTCTGCCCTCGCACTGCTGCCCTGGGCTCGGCGCGGGCTCTTCTCTTTGGCCAGCCC 348

100

Db 24 LeuLeuGlnLeuLeuLeuGlyProAlaArgGly-----PheGlyValAsnGly11 40

[illegible][illegible]

QY 349 GACTTCTCCTACAAGCGCAGCAAATTGCAAGCCCCATCCCGCCAACTGCAGCTGTGCCAC 408






Db 41 Glu-----GluArgArgCysAspProile-----ArgIleSerMetCysGln 54

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QY 409 GGCATCGAATACCAGAACATCGGGCTGCCCAACCTGCTGGGCCACGAGACCATGAAGGAG 468

[illegible]

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55 AsnLeuGlyTyrAsnValThrLysMetProAsnLeuValGlyHisGluLeuGlnThrAsp 74

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Qy 469 GTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCGGACACC 528

Db 75 AlaGluLeuGlnLeuThrThrPheThrProLeuIleGlnTyrGlyCysSerSerGlnLeu 94

**THE UNIVERSITY OF CHICAGO**

529 AAGAA GTTC NTGTG CTGGCTCTT CGCCCTCGCTCTG CTTAGACGAGACCATC 588

QY  
329 AAGAAAGTTCCTGTGCTCGCTCCTGGCCCGCTCGATGACCTAGACGAGACCATTG 588

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Db 95 GlnPhePheLeuCysSerValTyrValProMetCysThrGluLysIleAsnIleProIle 114









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Qy	574	CTAGCAGAGACCATCGACCATCGCTCTCGTGCAGGTGAAGACCGCTGCGCC	633
Db	117	LeuGluArgProIleProProCysArgSerLeuCysGluSerAlaArg---ValCysGlu	135
Qy	634	CCGCTCATGTCCGCTTCGGCTTCCCTGCGCCGACATGCTTGTGAGTGCACCGTTC	693
Db	136	LysLeuMetLysThrTyAsnPheAsnTrpProGluAsnLeuGluCysSerLysPhePro	155
Qy	694	-----CAGGACACGACGCTTTGTCATCCCTCCCTCGGTAGC	726
Db	156	ValHisGlyGlyGluAspLeuCysValAlaGluAsn-ThrThrSerSerAlaSerThrAl	175
Qy	727	AGCGACC-----ACCTCTGCCA	744
Db	175	aAlaThrProThrArgSerValAlaLysValThrThrArgLysHisGlnThrGlyValGl	195
Qy	745	GCCACCGAGGAAGCTCCAAAGGTATGTGAAGCTCGCAAAATAAAA	790
Db	195	uSerProHisArgAsnIleGlyPheValCysProValGlnLeuLys	210

RESULT 13

T31690

hypothetical protein F27E11.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 02-Mar-2001

C:Accession: T31690

R:Wamsley, P.; Keppler, D.

A:Submitted to the EMBL Data Library, July 1997

A:Description: The sequence of *C. elegans* cosmid F27E11.

A:Reference number: Z21069

A:Accession: T31690

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-605 <WAM>

A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CBSP:F27E11.3

A:Experimental source: strain Bristol N2; clone F27E11

C:Genetics:

A:Gene: CBSP:F27E11.3

A:Map position: 5

A:Introns: 28/3; 454/1; 520/1; 562/1

C:Superfamily: fruit fly frizzled protein

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Db      101 IleCysAlaIaProAspThrProLysLysGlnHisLysGlyHisHisLysAsn 120
QY      787 AAAAATGATGATGACAAC 804
Db      121 GlnAsnGlnAsnGlnAsn 126

RESULT 14
JE0315
low-density lipoprotein receptor-related protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JE0315
R:Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.
J. Biochem. 124, 784-789, 1998
A:Title: A novel low-density lipoprotein receptor-related protein with type II membrane
A:Reference number: JE0315; MUID:98429596; PMID:9756624
A:Accession: JE0315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1113 <TM>
A:Cross-references: UNIPROT:Q9Z319; DDBJ:AB013874; NID:G3869144; PIDN:BAA34371.1; PID:G
C:Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor lig
F:337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:869-1097/Domain: trypsin homology <TRY>

Alignment Scores:
Pred. No.: 7 83e-07 Length: 1113
Score: 220.50 Matches: 56
Percent Similarity: 42.49% Conservative: 26
Best Local Similarity: 29.02% Mismatches: 84
Query Match: 6.15% Indels: 27
DB: 2 Gaps: 6

US-08-949-904A-1 (1-2027) x JE0315 (1-1113)

QY      307 TGCCTGGGCTCGGCGCGCGGCTTCTCTCTTTTGGCCAGCCGACTTCTCTACAAGCGC 366
Db      501 CysValGluSerCysAlaGlySerSerLeuLeuCysAspSerSerLeuSerAsnCys 520
QY      367 AGCAATTGCAAGCCCATCCGGCCCACTCGAGCTGTGCCACCGCATCGAATACCAGAAC 426
Db      521 SerGlnCysGluProfile-----ThrLeuGluLeuCysMetAsnLeuLeuTyrAsnHis 538
QY      427 ATCGGGCTGCCACCTGCTGGGCCACGACCATGAAGGAG-----GTGCTGGAGCAG 480
Db      539 ThrHisTyrProAsnTyrLeuGlyHisArgThrGlnLysGluAlaSerIleSerTrpGlu 558
QY      481 GCCGGCTTGGATCCCGCTGGTCATGAACGACGTGCCACCCGGACACCAAGAAGTTCCTG 540
Db      559 SerSerLeuPheProAlaLeuValGlnThrAsnCysTyrLysTyrLeuMetPhePheAla 578
QY      541 TGCTCGCTTTCGCCCGCCGCTCGCTCGATGACCTAGACGAGACCATTCAGCGCATGCCAC 600
Db      579 CysThrIleLeuValProLysCysAspValAsnThrGlyGlnArgIleProProCysArg 598
QY      601 TCGCTCTCGCTGCAAGGTGAAGGACCGCTGCCCGCCGTCATGTCGGCTTCGGCTTCCCC 660
Db      599 LeuLeuCysGluHisSerLysGluArgCysGluSerValLeuGlyIleValGlyLeuGln 618
QY      661 TGGCCCCACATGCTTGAGTCGCACCGCTTTCCTCCCGAG-----GACAAACGACCTTTGC 711
Db      619 TrpProGluAspThrAspCysAsnGlnPheProGluLusSerSerAspAsnGlnThrCys 638
QY      712 ATCCCCCTCGCTAGACGCGACCACTCTCTCGCCAGCCACCGAGGAAGCTCCAAAGGTATGT 771
Db      639 Leu---LeuProAsnGluAsp-----ValGluGluCysSerProSerHis 652

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Search completed: September 1, 2005, 09:39:26  
Job time : 75.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2005, 09:39:32 ; Search time 631.5 Seconds  
(without alignments)  
2528.202 Million cell updates/sec

Title: US-08-949-904A-1

Perfect score: 3585  
Sequence: 1 GAATTCGGCCTTCATGGCCT.....AAAAAAGCGCGCGC 2027

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 3548624

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO spool\_p/US08949904/runat\_01092005\_102615\_21339/app.query.fasta\_1.2183  
-DB=PublishedApplications\_AA -QWMSFASTAN -SUFFIX=rapb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US08949904 @CGN 1 1 304 @runat\_01092005\_102615\_21339  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pcp.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pcp.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1976.5	55.1	377	14	US-10-106-698-6382
2	1594	44.5	295	8	US-08-949-904-2
3	1594	44.5	295	14	US-10-177-293-142
4	1594	44.5	295	15	US-10-295-027-1345
5	1594	44.5	295	16	US-10-783-528-107
6	1594	44.5	295	17	US-10-847-972-78
7	1594	44.5	295	17	US-10-432-256-2
8	1590	44.4	295	9	US-09-978-295A-415
9	1590	44.4	295	9	US-09-978-697-415
10	1590	44.4	295	9	US-09-978-192A-415
11	1590	44.4	295	9	US-09-999-832A-415
12	1590	44.4	295	10	US-09-978-189-415
13	1590	44.4	295	10	US-09-978-608A-415
14	1590	44.4	295	10	US-09-978-585A-415
15	1590	44.4	295	10	US-09-978-191A-415
16	1590	44.4	295	10	US-09-978-403A-415
17	1590	44.4	295	10	US-09-978-564A-415
18	1590	44.4	295	10	US-09-999-833A-415
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20	1590	44.4	295	10	US-09-978-824-415
21	1590	44.4	295	10	US-09-978-824-415
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28	1590	44.4	295	10	US-09-978-187B-415
29	1590	44.4	295	10	US-09-978-643A-415
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32	1590	44.4	295	10	US-09-978-681A-415
33	1590	44.4	295	10	US-09-978-194A-415
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35	1590	44.4	295	10	US-09-978-299A-415
36	1590	44.4	295	10	US-09-978-544A-415
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44	1590	44.4	295	14	US-10-013-929A-415
45	1590	44.4	295	14	US-10-016-177A-415

ALIGNMENTS

RESULT 1  
US-10-106-698-6382  
; Sequence 6382, Application US/10106698  
; Publication No. US20030103690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106.698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8584  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 6382  
; LENGTH: 377

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (127)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-6382

## Alignment Scores:

Pred. No.: 1.31e-127 Length: 377  
Score: 1976.50 Matches: 370  
Percent Similarity: 98.93% Conservative: 0  
Best Local Similarity: 98.93% Mismatches: 2  
Query Match: 55.13% Indels: 2  
DB: 14 Gaps: 1

US-08-949-904A-1 (1-2027) x US-10-106-698-6382 (1-377)

QY 24 TCATTCTGCTCCCGGGTTCGAGAGCCCGCGAGCTGGCGGGCTTCAGCGCTCGC 83  
Db 5 SerPheCysSerProGlySerGluProGlyAlaAlaArgGlyLeuAlaAlaProArg 24  
QY 84 CCGCGCT---CCTCCCGGTGTCCTCCCGCGCCCGCGCGCTGCGAGCTTTT 140  
Db 25 Pro-ArgCysProProGlyValProLeuLeuArgAlaProAlaAlaGlyCysGlnLeuPh 44  
QY 141 CGGGGCGCGAGTCGACCCAGCGAGAGAGCGGCGCGGCAAGCTCGAACTCGGCG 200  
Db 44 eGlyAlaProSerArgThrGlnArgArgGluAlaArgAspLysLeuGluLeuArgPr 64  
QY 201 GCTCGCCCTTCCCGGCTCCGCTCCCTGCTCCGCTCGGGTCCGCGCGCCACCATGCT 260  
Db 64 oProArgProSerProAlaProLeuProLeuProProArgGlyArgAlaProThrMetLe 84  
QY 261 GCAGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320  
Db 84 uGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysLeuGlySerAl 104  
QY 321 GCGCGGCTTCTCTTTGGCCAGCCGACTTCTTCAAGCGAGCAATTCGAAGCC 380  
Db 104 aArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrlsA-gSerAsnCysLysPr 124  
QY 381 CATCCCGGCCACCTCGAGCTGTCAGCGGCATCCGAATACCAAGACATCGGCTGCCAA 440  
Db 124 ollePro\*\*\*AenLeuGlnLeuCysHisGlyIleGluTyrlsGlnAsnMetArgLeuProAs 144  
QY 441 CTGCTGGGCCACGAGACCATCAAGAGGTGTGAGCAGCGCGCGCTTGGATCCCGCT 500  
Db 144 nLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIleProLe 164  
QY 501 GGTATGAGAGTGCACCCCGGACACAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTG 560  
Db 164 uValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAlaProVa 184  
QY 561 CTGCTCGATGACCTAGACGAGACCATCCAGCATCCGCTCGCTCGCTCGCTCGAGTGA 620  
Db 184 lCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGlnVally 204  
QY 621 GCACCGCTGCGCGCGCGCTCATGCTCGCGCTTCCGCTTCCGCTGCGCGCGAGCTTGA 680  
Db 204 sAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeuGluCy 224  
QY 681 CGACCGTTTCCCGAGGACAGACTTTGATTCCTCGCTGCTGCTGCTGCTGCTGCTGCT 740  
Db 224 sAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHisLeuLe 244  
QY 741 GCACGCGCCGAGGAGCTCCAAAGGTATGTGAAGCTGCAAAATAAAATGATGATGA 800  
Db 244 uProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAspAs 264  
QY 801 CAACGACATAATGGAAGCGCTTTGTAATAATGATTTGCACTGAAATAAAGTAGGAAGA 860  
Db 264 pAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysValLysG 284

QY 861 GATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGACAGACCATTTA 920  
Db 284 uIleThrTyrlsIleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThrIleTy 304  
QY 921 CAAGCTGAACGGTGTTCGAAAGGAGCCTCAAGAAATCGGTGCTGTGGCTCAAAAGACAG 980  
Db 304 rLysLeuAsnGlyValSerGluArgAspLeuLysSerValLeuTrpLeuLysAspSe 324  
QY 981 CTTGCAGTGCACCTGTGAGGAGATCAACGACATCAACCGCGCCTATCTTGGTCATGGGACA 1040  
Db 324 rLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlsLeuValMetGlyGl 344  
QY 1041 GAAACAGGTCGGGAGCTGTCATCCTCGTGAAGCGGTGGCAAGAGGGCGCAGAGAGA 1100  
Db 344 nLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGlnArgGl 364  
QY 1101 GTTCAAGCGCATCTCCGCGAGCATCCGCAAGCTGCAGTGC 1140  
Db 364 uPheLysArgIleSerArgSerIleArgLysLeuGlnCys 377

## RESULT 2

US-08-949-904-2  
; Sequence 2, Application US/08949904  
; Publication No. US20030175855A1  
; GENERAL INFORMATION:  
; APPLICANT: LaVallie, Edward  
; APPLICANT: Racie, Lisa  
; TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENETICS INSTITUTE, INC.  
; STREET: 87 CAMBRIDGE PARK DRIVE  
; CITY: CAMBRIDGE  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,904  
; FILING DATE: October 15, 1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAZAR, STEVEN R.  
; REGISTRATION NUMBER: 32,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8260  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-949-904-2

## Alignment Scores:

Pred. No.: 2.84e-101 Length: 295  
Score: 1594.00 Matches: 295  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 44.46% Indels: 0  
DB: 8 Gaps: 0

US-08-949-904A-1 (1-2027) x US-08-949-904-2 (1-295)

QY 256 ATGCTGAGGCGCCCTGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315  
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Db      1 MetLeuGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20
Qy      316 TCGCGCGCGGGCTCTTCTCTTTGGCCAGCCCGACTTCTCTACAGCGCGAGCAATTGC 375
Db      21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCyS 40
Qy      376 AGCCCATCCCGCCCAACTGCGAGCTGTGCCAGCATCGAATACAGAACATCGCGGTG 435
Db      41 LysProIleProAlaAsnLeuGlnLeuCySHisGlyIleGluTyrGlnAsnMetArgLeu 60
Qy      436 CCCAACTCTGCGGCCACGAGACCATGAAGGAGGTCTGGAGCAGCCGCGCTTGATC 495
Db      61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
Qy      496 CCGCTGTGTCATGAAGCAGTCCACCCGCGACACCAAGAAGTCTCTGTCTCGCTTCGCG 555
Db      81 ProLeuValMetLysGlnCySHisProAspThrLysPheLysPheLeuCySerLeuPheAla 100
Qy      556 CCGCTGTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTCGGTGCAG 615
Db      101 ProValCySLeuAspLeuAspGluThrIleGlnProCySHisSerLeuCySValGln 120
Qy      616 GTGAAGGACCGCTGCGCCCGGTCTATGTCGGCTTCGGCTTCCCTGGCCCGACATGCTT 675
Db      121 ValLysAspArgCySAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
Qy      676 GAGTGGACCGTTTCCCCCAGGACCATTTGCATCCCCCTCGCTAGCAGCACAC 735
Db      141 GluCySAspArgPheProGlnAspAsnLeuCySValIleProLeuAlaSerSerAspHis 160
Qy      736 CTCCTGCCACGCCAGGAAAGCTCCAAAGGTATGTGAAGCTGTGAAGCTGCAGAAATATAAATGAT 795
Db      161 LeuLeuProAlaThrGluGluAlaProLysValCySAlaCySLeuAsnLysAsnAsp 180
Qy      796 GATGACAAAGCATATGAAGCGTTTGTAAATGATTTTGCACCTGAAATATAAAGTG 855
Db      181 AspAspAsnAspIleMetGluThrLeuCySAsnAspPheAlaLeuLysIleLysVal 200
Qy      856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTGGAGACCAAGAGCAAGACC 915
Db      201 LysGluIleThrTyrIleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
Qy      916 ATTTACAAGCTGAACGGTGTGTCGAAAGGAGCACTCGAAGAAATCGGTGCTGTGCTCAAA 975
Db      221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
Qy      976 GACAGCTTCGATGACCTGTGAGGAGATGAAGCATCAACGCGCCCTATCTGTGTCATG 1035
Db      241 AspSerLeuGlnCySThrCySLeuGluMetAsnAspIleAsnAlaProTyrLeuValMet 260
Qy      1036 GGACAGAAACAGGGTGGGAGCTGGTGATCACCTCGGTGAACGGTGGCAGAAAGGGCAG 1095
Db      261 GlyGlnLysGlnGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
Qy      1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db      281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCyS 295
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## RESULT 3

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US-10-177-293-142
; Sequence 142, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
```

```
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; PREVENTION, AND THERAPY OF BREAST CANCER
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-142

Alignment Scores:
Pred. No.: 2,84e-101 Length: 295
Score: 1594.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.46% Indels: 0
DB: 14 Gaps: 0

US-08-949-904A-1 (1-2027) x US-10-177-293-142 (1-295)

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Db      21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCyS 40
Qy      376 AAGCCATCCCGCCCAACTGCGAGCTGTGCCAGCATCGAATACAGAAATCGCGGTG 435
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Qy      436 CCCAACTCTGCGGCCACGAGACCATGAAGGAGGTCTGGAGCAGCCGCGCTTGATC 495
Db      61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
Qy      496 CCGCTGTGTCATGAAGCAGTGCACCCGCGACACCAAGAAGTCTCTGTGCTCGCTTCGCG 555
Db      81 ProLeuValMetLysGlnCySHisProAspThrLysLysPheLeuCySerLeuPheAla 100
Qy      556 CCGCTGTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTCGGTGCAG 615
Db      101 ProValCySLeuAspLeuAspGluThrIleGlnProCySHisSerLeuCySValGln 120
Qy      616 GTGAAGGACCGCTGCGCCCGGTCTATGTCGGCTTCCGCTTCCCTGGCCCGACATGCTT 675
Db      121 ValLysAspArgCySAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
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QY 796 GATGACACGACATATGGAACGCTTCTTAAATATGTTTGGCACTGAATAAAGTG 855
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Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295
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## RESULT 4

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US-10-295-027-1345
; Sequence 1345, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-21
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; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-13
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1345
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1345
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Pred. No.: 2,84e-101 Length: 295
Score: 1594.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.46% Indels: 0
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US-08-949-904A-1 (1-2027) x US-10-295-027-1345 (1-295)

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QY 436 CCCAACCTGCTGGGCCACGAGACCATGAAGAGAGTGTGGAGAGCGCGCGCTTGGATC 495
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
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QY 556 CCGCTGCTCGATGACCTAGACGAGACCATCGACCATGCCACTCGCTCTGCTGCTGCGAG 615
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Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
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QY 976 GACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACAGCGGCCCTATCTGTGTCATG 1035
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Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuValGln 120  
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 QY 796 GATGACAAACGACATAATGAAACGCTTTGTAAAAATGATTTTGCACTGAAATAAAGTG 855  
 Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200  
 QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTGGAGACCAAGACGAGACC 915  
 Db 201 LysGluIleThrTyrIleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220  
 QY 916 ATTTACAAAGCTCAACGGTGTGTCGAAAGGACCTGAAAGAAATCGGTGCTGGCTCAAA 975  
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 QY 976 GACAGCTTGCAGTGCACCTGTGAGAGATGAACGACATCAACGCGCCCTATCTGTCATG 1035  
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RESULT 7

US-10-432-256-2  
 ; Sequence 2, Application US/10432256  
 ; Publication No. US20050113291A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Applied Research Systems ARS Holding N.V.  
 ; TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma  
 ; FILE REFERENCE: EP 469 Y  
 ; CURRENT APPLICATION NUMBER: US/10/432,256  
 ; CURRENT FILING DATE: 2003-12-12  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-432-256-2

Alignment Scores:

Pred. No.: 2,846-101 Length: 295  
 Score: 1594.00 Matches: 295  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 44.46% Indels: 0  
 DB: 17 Gaps: 0

US-08-949-904A-1 (1-2027) x US-10-432-256-2 (1-295)

QY 256 ATGCTGCAGGCGCTGGCTCGTGTGCTTCTTCTCGCTCGCTCGCTCGCTCGCTGGC 315  
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 Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCys 40

QY 376 AAGCCATCCCGCCCAACCTGCAGCTGTGCCCGCATCGAATACCAAGAACATCGGCTG 435  
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 QY 436 CCCAACCTGTGGGCCACGAGACCATGAAGAGGTGTGGAGAGCGCGGCTTGGATC 495  
 Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80  
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 QY 556 CCGCTGTCTGTGATGACCTAGACGAGACCATCCAGCCATCCGCTGCTGCTGCTGCGAG 615  
 Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120  
 QY 616 GTGAAGGACCGCTCGCGCCCGTCTATGTCCGCTTCCGCTTCCCTCGCTCGCTGCTT 675  
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 QY 1096 AGAGAGTTCAACGCGATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140  
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RESULT 8

US-09-978-295A-415  
 ; Sequence 415, Application US/09978295A  
 ; Patent No. US20020156006A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-05-05  
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PRIOR APPLICATION NUMBER: 60/084441



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;	PRIOR APPLICATION NUMBER:	60/081955
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;	PRIOR APPLICATION NUMBER:	60/084643
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;	PRIOR APPLICATION NUMBER:	60/085339
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;	PRIOR FILING DATE:	1998-05-13











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## RESULT 12

US-09-978-189-415  
; Sequence 415, Application US/09978189  
; Publication No. US20030004102A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978.189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR FILING DATE: 1998-03-31  
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; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328





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; Publication No. US2003004963A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-415

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Best Local Similarity: 99.66% Mismatches: 1
Query Match: 44.35% Indels: 0
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; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
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PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2005, 09:26:23 ; Search time 51 Seconds  
(without alignments)  
5933.869 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-O=/cgn2\_1/USPTO spool\_p/US08949904/runat\_01092005\_102613\_21270/app\_query.fasta\_1.2183  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1586	44.2	295	4	US-09-148-545-179 Sequence 179, App
2	1586	44.2	296	4	US-09-148-545-237 Sequence 237, App
3	1557	43.4	295	4	US-08-937-067-2 Sequence 2, Appli
4	1140	31.8	212	4	US-08-937-067-4 Sequence 4, Appli
5	624	17.4	317	4	US-08-937-067-6 Sequence 6, Appli
6	624	17.4	317	4	US-09-949-016-6300 Sequence 6300, Ap
7	614.5	17.1	305	4	US-09-949-016-7706 Sequence 7706, Ap
8	608	17.0	313	4	US-09-514-885-1 Sequence 1, Appli
9	608	17.0	313	4	US-09-949-016-6299 Sequence 6299, Ap
10	606.5	16.9	314	4	US-08-937-067-7 Sequence 7, Appli
11	606	16.9	313	4	US-09-546-043-3 Sequence 3, Appli
12	606	16.9	338	4	US-09-546-043-4 Sequence 4, Appli

13	590	16.5	113	4	US-09-087-031E-24 Sequence 24, Appl
14	589	16.4	313	4	US-09-087-031E-4 Sequence 4, Appli
15	587.5	16.4	314	4	US-09-087-031E-3 Sequence 3, Appli
16	498	13.9	295	3	US-08-893-654B-6 Sequence 6, Appli
17	478	13.3	267	4	US-09-546-043-7 Sequence 7, Appli
18	459.5	12.8	246	4	US-09-546-043-6 Sequence 6, Appli
19	433.5	12.1	280	3	US-08-893-654B-4 Sequence 4, Appli
20	407	11.4	281	3	US-08-893-654B-2 Sequence 2, Appli
21	382	10.7	195	4	US-09-546-043-5 Sequence 5, Appli
22	353	9.8	109	4	US-09-087-031E-19 Sequence 19, Appli
23	279	7.8	685	4	US-08-937-067-14 Sequence 14, Appli
24	277.5	7.7	585	4	US-08-937-067-9 Sequence 9, Appli
25	275.5	7.7	572	4	US-08-937-067-13 Sequence 13, Appli
26	274	7.6	371	4	US-09-949-016-7544 Sequence 7544, Ap
27	274	7.6	537	4	US-08-937-067-11 Sequence 11, Appli
28	269.5	7.5	565	4	US-08-937-067-8 Sequence 8, Appli
29	266	7.4	323	3	US-08-878-474-7 Sequence 7, Appli
30	260.5	7.3	114	4	US-09-087-031E-15 Sequence 15, Appli
31	260	7.3	318	3	US-08-878-474-3 Sequence 3, Appli
32	259.5	7.2	325	3	US-08-878-474-9 Sequence 9, Appli
33	259.5	7.2	325	4	US-09-976-594-479 Sequence 479, App
34	251	7.0	55	4	US-09-621-976-3894 Sequence 3894, Ap
35	250.5	7.0	229	4	US-09-546-043-8 Sequence 8, Appli
36	244.5	6.8	114	4	US-09-087-031E-20 Sequence 20, Appli
37	241	6.7	115	4	US-09-087-031E-10 Sequence 10, Appli
38	237	6.6	114	4	US-09-087-031E-21 Sequence 21, Appli
39	235	6.6	114	4	US-09-087-031E-12 Sequence 12, Appli
40	231	6.4	102	4	US-09-959-392-20 Sequence 20, Appli
41	229.5	6.4	112	4	US-09-087-031E-17 Sequence 17, Appli
42	228	6.4	111	4	US-09-087-031E-14 Sequence 14, Appli
43	227.5	6.3	1042	4	US-09-959-392-2 Sequence 2, Appli
44	227	6.3	111	4	US-09-087-031E-9 Sequence 9, Appli
45	226	6.3	891	4	US-09-252-991A-30624 Sequence 30624, A

ALIGNMENTS

RESULT 1  
US-09-148-545-179  
; Sequence 179, Application US/09148545  
; Patent No. 6590075  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: PZ001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: PCT/US98/04482  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
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; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
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; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23





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EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,598
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,613
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,582
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047,596
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EARLIER	FILING DATE:	1997-05-23
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EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/043,671
EARLIER	FILING DATE:	1997-04-11
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EARLIER	APPLICATION NUMBER:	60/043,669
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EARLIER	APPLICATION NUMBER:	60/056,886
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EARLIER	APPLICATION NUMBER:	60/056,877
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,889
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,893
EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,879
EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056,894
EARLIER	FILING DATE:	1997-08-22

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3	EARLIER APPLICATION NUMBER: 60/056,636
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,874
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,910
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,864
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,631
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,845
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,892
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/047,595
18	EARLIER FILING DATE: 1997-05-23
19	EARLIER APPLICATION NUMBER: 60/057,761
20	EARLIER FILING DATE: 05-Sep-1997
21	EARLIER APPLICATION NUMBER: 60/047,599
22	EARLIER FILING DATE: 1997-05-23
23	EARLIER APPLICATION NUMBER: 60/047,588
24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/047,585
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,586
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,590
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,594
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,589
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,593
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,614
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/043,578
40	EARLIER FILING DATE: 1997-04-11
41	EARLIER APPLICATION NUMBER: 60/043,576
42	EARLIER FILING DATE: 1997-04-11
43	EARLIER APPLICATION NUMBER: 60/047,501
44	EARLIER FILING DATE: 1997-05-23
45	EARLIER APPLICATION NUMBER: 60/043,670
46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/056,632
48	EARLIER FILING DATE: 1997-08-22
49	EARLIER APPLICATION NUMBER: 60/056,664
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/056,876
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,881
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,909
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,875
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/048,964
60	EARLIER FILING DATE: 1997-06-06
61	EARLIER APPLICATION NUMBER: 60/057,650
62	EARLIER FILING DATE: 1997-09-05
63	EARLIER APPLICATION NUMBER: 60/056,884
64	EARLIER FILING DATE: 1997-08-22
65	NUMBER OF SEQ ID NOS: 280
66	SOFTWARE: PatentIn Ver. 2.0
67	SEQ ID NO 237





ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,067  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20018.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-937-067-6

Alignment Scores:  
Pred. No.: 1,18e-43 Length: 317  
Score: 624.00 Matches: 132  
Percent Similarity: 57.01% Conservative: 51  
Best Local Similarity: 41.12% Mismatches: 97  
Query Match: 17.41% Indels: 41  
DB: 4 Gaps: 7

US-08-949-904A-1 (1-2027) x US-08-937-067-6 (1-317)

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QY 231 GCCCCTCGGGTCCGCGCCACCATGCTGCAGGCGCCCTGCTGCTGCTCTT 290  
DB 25 AlaProAlaArgCysGluGluTyrAspTyrTyrGly----- 36  
QY 291 CCTCGCTCGCACTGCTGCTGGGCTCGGCGCGGCTCTTCTCTTTGGCCAGCCGA 350  
DB 37 -----TrpGlnAlaGlu 40  
QY 351 CTTCTCTACAGCCAGCAATGTCAGCC-----ATCCGCGCAACT 395  
DB 41 ProLeu-HisGlyArgSerTyrSerLysProGlnCysLeuAspIleProAlaAspLe 60  
QY 396 CGAGCTGCGCCAGCATCGATACCAAGACATCGGCTGCCACCTGCTGGGCGCAGA 455  
DB 60 uProLeuCysHisThrValGlyTyrLysArgMetArgLeuProAsnLeuGluHisG 80  
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DB 80 uSerLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCy 100  
QY 516 CCACCGGACACCAAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575  
DB 100 sHisSerAspThrGlnValPheLeuLeuCysSerLeuPheAlaProValCys-----Le 117  
QY 576 AGACGAGACCATCCAGCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635  
DB 117 uAspArgProIleTyrProCysArgSerLeuLeuAlaValaValaGlyCysAlaPr 137  
QY 636 GGTCAATGCGCGCTTCGCGCTTCCTCCCTCGCCGCGCATGCTTGAGTCGCGACCGTTC 695

DB 137 oLeuMetGluAlaTyrGlyPheProTrpProGluMetLeuHisCysHisLysPheProLe 157  
QY 696 GACAAACGACCTTTGCTATCCCTCGCTAGCAGGACCACTCTCTGCGGCGCCAGGAG 755  
DB 157 uAspAsnAspLeuCysIleAlaValGlnPheGlyHis-----LeuProAlaThr----- 173  
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DB 174 -AlaProValThrLysIleCysAlaGlnCysGluMetGluHisSerAlaAspGly-- 192  
QY 807 CATAATGAAACGCTTTGTAATAATGATTTTGCACCTGAAATAATAAGTGAAGGAGATAAC 866  
DB 193 -LeuMetGluGlnMetCysSerSerAspPheValValLysMetArgIleLysGluIleLy 212  
QY 867 CTACATCAACCGAGATACCAAAATCATCTCTGGAACCAAGAGCAAGACCATTTACAAGCT 926  
DB 212 sIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLeuLeuLysPr 232  
QY 927 GAACGGTGTGTCGAAAGGACCTGAAATAATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 986  
DB 232 oGlyProLeuLysArgLysAspThrLysArgLeuValLeuHisMetLysAsnGlyAlaGl 252  
QY 987 GTGCACCTGTGAGGAGATGAACGACATCAACGCCCTCTATCTGCTCATGGGACAGAAACA 1046  
DB 252 yCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArgLysVa 272  
QY 1047 GGTGGGAGCTGTGATCACCTCGTGAACCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGT 1106  
DB 272 lAspGlyGlnLeuLeuMetAlaValTyrArgTrpAspLysLysAsnLysGluMetLy 292  
QY 1107 G 1107  
DB 292 s 292

## RESULT 6

US-09-949-016-6300  
; Sequence 6300, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR FILING DATE: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6300  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6300

Alignment Scores:  
Pred. No.: 1,18e-43 Length: 317  
Score: 624.00 Matches: 132  
Percent Similarity: 57.01% Conservative: 51  
Best Local Similarity: 41.12% Mismatches: 97  
Query Match: 17.41% Indels: 41  
DB: 4 Gaps: 7

US-08-949-904A-1 (1-2027) x US-09-949-016-6300 (1-317)

QY 171 GCGGCGCGGACAGCTCGAAGCTCGGCGGCTCGCCCTTCCTCCCGGCTCGCTCCCTCT 230  
DB 5 AlaAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuGlyAlaLeuHisTrp 24





Db 214 LysLysLysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArgLeuValLeu 233  
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Db 234 HisMetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPhe 253  
Qy 1027 CTGGTTCATGGACAGAAACAGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAG 1086  
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Qy 1087 AAGGGGCACAGAGATTCAAG 1107  
Db 274 LysLysAsnLysGluMetLys 280  
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; Sequence 1, Application US/09514885  
; Patent No. 6556461  
; GENERAL INFORMATION:  
; APPLICANT: D'Armiesto, Jeanine  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE  
; PULMONARY DISEASE  
; FILE REFERENCE: 58483.8pp  
; CURRENT APPLICATION NUMBER: US/09/514,885  
; CURRENT FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
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; TYPE: PRT  
; ORGANISM: Human  
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Qy 448 GCCCAGCAGACCATGAAGAGGTGCTGGAGCGCGCGCTTGGATCCCGTGGTGCATG 507  
Db 82 GluHisGluThrMetAlaGluValLysGlnAlaSerSerTrpValProLeuLeuAsn 101  
Qy 508 AGCAGTGCACCCGACACCAAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 567  
Db 102 LysAsnCysHisAlaGlyThrGlnValPheLeuCysSerLeuPheAlaProValCys--- 120  
Qy 568 GATGACCTAGACGAGACCATGCAGCCATCCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627  
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Qy 928 AACGCTGTGTCGAAAGGACCTGAAGAAATCGGTGCTGTGCTCAAAAGACAGCTTGCAG 987  
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Qy 988 TGCACCTGTGAGGAGATGAACACATCAACGGCGCCCTATCTGCTCATCGGACAGAAACAG 1047  
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RESULT 9  
US-09-949-016-6299  
; Sequence 6299, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6299  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6299  
Alignment Scores:  
Pred. No.: 2,538-42 Length: 313  
Score: 608.00 Matches: 123  
Percent Similarity: 59.16% Conservative: 61  
Best Local Similarity: 39.55% Mismatches: 107  
Query Match: 16.96% Indels: 20  
DB: 4 Gaps: 6  
US-08-949-904A-1 (1-2027) x US-09-949-016-6299 (1-313)  
Qy 241 GGTGCGCGCCACCATGCTCAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Db 4 GlyArgSerGluGlyGlyArgGlyAlaLeuGlyValLeuLeuAlaLeuGlyAlaAla 23

```
QY 301 CACTGCTGCTGGCTCGCGCGC-----GGG 327
Db 24 LeuLeuAlaValGlySerAlaSerGluTyrAspTyrValSerPheGlnSerAspIleGly 43
QY 328 CTCCTCTCTTTGGCCAGCCGACCTTCCTACAGCGCAGCAATTGCAAGCCCATCCCG 387
Db 44 ProTyrGlnSerGlyArg-----PheTyrThrLysProGlnCysValAspIlePro 61
QY 388 GCCAACCTGCAGCTGTGCCAGCGCATCGAATACCAAGACATCGCGCTGCCCAACCTGCTG 447
Db 62 AlaAspLeuArgLeuCysHisAsnValGlyTyrLysLysMetValLeuProAsnLeuLeu 81
QY 448 GCCACGAGACCATGAAGAGAGTGTGGAGCGAGCGCGGCTTGATCCCGTGTGTATG 507
Db 82 GluHisGluThrMetAlaGluValLysGlnGlnAlaSerSerTrpValProLeuLeuAsn 101
QY 508 AAGCAGTGCACCGGACACCAAGATTTCCTGCTGCTCGCTTCCGCCCGCTGCGCTC 567
Db 102 LysAsnCysHisAlaGlyThrGlnValPheLeuCysSerLeuPheAlaProValCys--- 120
QY 568 GATGACCTAGACGAGACCATCGACGATCGCTCGCTGCTGCGTGCAGGTGAAGACCGC 627
Db 121 -----LeuAspArgProIleTyrProCysArgTrpLeuCysGluAlaValArgAspSer 138
QY 628 TCGCGCCCGGTGATGTCGCGCTTCGGCTTCCCTCGCGCGACATGCTTGAGTGCGACGCT 687
Db 139 CysGluProValMetGlnPhePheGlyPheTyrTrpProGluMetLeuLysCysAspLys 158
QY 688 TTCCTCCAGGACAAAGCCTTTGATGTCATCCCTCGCTAGCAGGACCATCTCTGCCAGCC 747
Db 159 PhePro---GluGlyAspValCysIleAlaMetThrProProAsnAlaThrGluAlaSer 177
QY 748 ACCGAGGAGCTCCAAAGGTATGTGAAGCTGCTCAAAAATAAAATGATGATGACACACG 807
Db 178 LysProGlnGlyThrThrValCysProProCysAspAsnGluLeuLysSerGlu---Ala 196
QY 808 ATAATGGAACCTTTGTAATAATGATTTTGACTGAAATAATAAGTGAAGAGATAACC 867
Db 197 IleIleGluHisLeuCysAlaSerGluPheAlaLeuArgMetLysIleLysGluValLys 216
QY 868 TATACCAACCGAGATACCAAAATCATCTGGAGACCAAGACAGACCATTTTACAAGCTG 927
Db 217 LysGluAsnGlyAspLysIleVal-----ProLysLysLysLysProLeuLysLeu 234
QY 928 AACGGTGTGTCGAAAGACCTGAAGAAATCGTGTGCTGCTGCTCAAAAGACAGCTTGCAG 987
Db 235 GlyProIleLysLysAspLeuLysLysLeuValLeuLysAsnGlyAlaAsp 254
QY 988 TGCACCTGTGAGGAGATGAACACATCAACGCGCCCTATCTGGTATCGGACAGAAACAG 1047
Db 255 CysProCysHisGlnLeuAspAsnLeuSerHisHisPheLeuIleMetGlyArgLysVal 274
QY 1048 GGTGGGGAGCTGTGATCACTCGTGAAGCGGTGCGAGAGGGGCGCAGAGAGTTCAAG 1107
Db 275 LysSerGlnTyrLeuLeuThrAlaIleHisLysTrpAspLysLysAsnLysGluPheLys 294
QY 1108 CGCATCTCCCGCAGCATCGCAAGCTGCAGTGC 1140
Db 295 AsnPheMetLysLysMetLysAsnHisGluCys 305
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```
RESULT 10
US-08-937-067-7
Sequence 7, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Unanaky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-067-7
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Alignment Scores:
Pred. No.: 3,37e-42 Length: 314
Score: 606.50 Matches: 124
Percent Similarity: 58.65% Conservative: 59
Best Local Similarity: 39.74% Mismatches: 102
Query Match: 16.92% Indels: 27
DB: 4 Gaps: 7
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US-08-949-904A-1 (1-2027) x US-08-937-067-7 (1-314)
QY 238 CGGGGTTCGCGCGCCACGATGCTGCAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
Db 11 ArgGlyAlaLeuLeuGlyValLeuLeuAlaLeuGlyAlaLeuLeu----- 26
QY 298 TCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
Db 27 -----AlaValGlySerAlaSerGluTyrAspTyrValSerPheGlnSerAspIle 43
QY 325 GGGCTCTCTCTTTGGCCAGCCGACCTTCCTACAGCGCAGCAATTGCAAGCCCATC 384
Db 44 GlyProTyrGlnSerGlyArg-----PheTyrThrLysProGlnCysValAspIle 61
QY 385 CCGGCCAACCTGCAGCTGTGCCAGCGCATCGAATACCAAGACATCGCGCTGCCCAACCTG 444
Db 62 ProAlaAspLeuArgLeuCysHisAsnValGlyTyrLysLysMetValLeuProAsnLeu 81
QY 445 CTGGCCACGAGACCATGAAGAGTGTGGAGCGCGCGCTTGATCCCGTGTGTC 504
Db 82 LeuGluHisGluThrMetAlaGluValLysGlnGlnAlaSerSerTrpValProLeuLeu 101
QY 505 ATGAAGCAGTGCACCGCGGACCAAGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
Db 102 AsnLysAsnCysHisAlaGlyThrGlnValPheLeuCysSerLeuPheAlaProValCys 121
QY 565 CTCGATGACCTAGACGAGACCATCCAGCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
Db 122 -----LeuAspArgProIleTyrProCysArgTrpLeuCysGluAlaValArgAsp 138
QY 625 CGCTGCGCCCGGTGATGTCGCGCTTCGGCTTCCCTGCGCGACATGCTTGAGTGCGAC 684
Db 139 SerCysGluProValMetGlnPhePheGlyPheTyrTrpProGluMetLeuLysCysAsp 158
QY 685 CGTTTCCCGCCAGGACACGACCTTTTGGATCCCTCGCTAGCAGGACCATCTCTCTGCA 744
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US-08-949-904A-1 (1-2027) x US-09-546-043-4 (1-338)
QY 271 GGCTCGCTGCTGCTCTTCCTCGCTCGCACTGCTGCTGGGCTCGCGCGCGGCTC 330
Db 16 GlyValLeuAlaLeuGlyGlyAlaSerGlyArgGlyLeuGlySerGluTyrAspTyr 35
QY 331 TTCCTCTTTGGCAGCCCGAC-----TTCTCTACAGCGC 366
Db 36 ValSerPhe---GlnSerAspIleGlyProTyrGlnSerGlyArgPheTyrThrLysPro 54
QY 367 AGCAATTGCAAGCCCATCCGCGCAACCTGCGCAGCTGTGCGCAGCATCGAATACCAGAAC 426
Db 55 ProGlnCysValAspIleProAlaAspLeuArgLeuCysHisAsnValGlyTyrLysLys 74
QY 427 ATGCGGCTGCCAACCTGCTGGGCCACGAGACCATGAAGGAGGTGCTGGAGAGCGCGC 486
Db 75 MetValLeuProAsnLeuLeuGluHisGluThrMetAlaGluValLysGlnAlaSer 94
QY 487 GCTTGGATCCCGTGTGATGAAGAGTGCACCCCGGACACCAAGAAGTTCTCTGTGCTCG 546
Db 95 SerTrpValProLeuLeuAsnLysAsnCysHisAlaGlyThrGlnValPheLeuCysSer 114
QY 547 CTCCTCGCCCGCTGCTGCTCGATGACCTAGACGAGACCATCCAGCCATCGCCTCGCTC 606
Db 115 LeuPheAlaProValCys-----LeuAspArgProIleTyrProCysArgTrpLeu 131
QY 607 TCGGTGAGGTGAAGACCGCTGCGCCCGGTGTCATGTCGCGCTTCGGCTTCCCGTGGGCC 666
Db 132 CysGluAlaValArgAspSerCysGluProValMetGlnPhePheGlyPheTyrTrpPro 151
QY 667 GATGCTTGAAGTGGACCGTTTCCCGAGGACAGACCTTTGATGATCCCGCTCGCTAGC 726
Db 152 GluMetLeuLysCysAspLysPhePro---GluGlyAspValCysIleAlaMetThrPro 170
QY 727 AGCGACCACTCTCTGCCACCCAGGAGGAGTCCAAAGGTATGTGAAGCTGCAAAAT 786
Db 171 ProAsnAlaThrGluAlaSerLysProGlnGlyThrValCysProCysAspAsn 190
QY 787 AAAAATGATGATGACAAACACATAATGGAACCGTTTGTAAAAATGATTTCACATGAAA 846
Db 191 GluLeuLysSerGlu---AlaIleIleGluHisLeuCysAlaSerGluPheAlaLeuArg 209
QY 847 ATAAAGTCAAGAGATACCTACATCAACCGAGATACCAAAATCATCTGAGACCAAG 906
Db 210 MetLysIleLysGluValLysLysGluAsnGlyAspLysLysIleVal-----ProLys 227
QY 907 AGCAAGACCATTTACAAGCTGAACGCTGTGTCGGAAGGACCTCAAGAAATCGTGTGTG 966
Db 228 LysLysLysProLeuLysLeuGlyProIleLysLysLysAspLeuLysLysLeuValLeu 247
QY 967 TGGCTCAAGACAGCTTGTCAGTGCACCTGTGTGAGAGATGAACGACATCAACGCGCCCTAT 1026
Db 248 TyrLeuLysAsnGlyAlaAspCysProCysHisGlnLeuAspAsnSerHisAspHe 267
QY 1027 CTGCTCATCGGACAGAAACAGCGGTGGGAGCTGGTATCACCCTCGTGAAGCGGTGGCAG 1086
Db 268 LeuIleMetGlyArgLysValLysSerGlnTyrLeuThrAlaIleHisLysTrpAsp 287
QY 1087 AAGGGCGCAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db 288 LysLysAsnLysGluPheLysAsnPheMetLysLysMetLysAsnHisGluCys 305

RESULT 13
US-09-087-031E-24
; Sequence 24, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
```

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; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087.031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087.031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050.417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-087-031E-24

Alignment Scores:
Pred. No.: 5,37e-41 Length: 113
Score: 590.00 Matches: 105
Percent Similarity: 93.81% Conservative: 1
Best Local Similarity: 92.92% Mismatches: 7
Query Match: 16.46% Indels: 0
DB: 4 Gaps: 0

US-08-949-904A-1 (1-2027) x US-09-087-031E-24 (1-113)
QY 373 TGCAGAGCCATCCCGGCCAACCTGCGAGCTGTGCGCAGCATCGAATACCAGAAACATGCGG 432
Db 1 CysLysProIleProAlaAsnLeuGlyLeuCysHisGlyIleGluTyrGlyAsnMetArg 20
QY 433 CTGCCCAACCTGCTGGGCCACGAGACCATGAAGAGAGGTGCTGGAGAGCGCGGCTTGG 492
Db 21 LeuProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlyAlaGlyAlaTrp 40
QY 493 ATCCCGCTGTGTCATGAAGCAGTGCACCGGACACCAAGAAAGTTCTCTGTGCTCGCTCTTC 552
Db 41 IleProLeuValMetLysGlyCysHisProAspThrLysLysPheLeuCysSerLeuPhe 60
QY 553 GCCCGCTGCTGCTCGATGACCTAGACGAGACCATCAGCCATGCCACTCGCTCGCTG 612
Db 61 AlaProValCysLeuAspAspLeuAspGluThrIleGlyProCysHisSerLeuCysMet 80
QY 613 CAGGTGAAGGACCGCTGCGCCCGCTGATGTCGCTTCCGCTTCCCGCTGCGCCGACATG 672
Db 81 GlyValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMet 100
QY 673 CTTGAGTGGACCGTTTCCCGCAGGACCAACGACCTTTGC 711
Db 101 LeuGluCysAspArgPheProGlyAspAsnAspLeuCys 113

RESULT 14
US-09-087-031E-4
; Sequence 4, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087.031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087.031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050.417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-4
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161 Pro---GluGlyAspValCysIleA

Db 161 Pro---GluGlyAspValCysIleAlaMetThrPro-----

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QY 751 GAGGAAGCTCCAAAG-----GTATGTGAAGCCTGCAGAAATAAAAAATGAT 795
Db ||||| ||| ||||| ||| |||:|:|
175 ThrGluAlaSerLysProGlyThrThrValCysProCysAspAsnGluLeuLys 194
QY 796 GATGACACGACATAATGGAACGCTTTGTAAAAATGATTTTGCACCTGAAAAATAAAGTG 855
Db :|:|:| ||| ||||| :|:|:| ||||| :|:|:| ||||| :|:|:| ||||| :|:|:|
195 SerGlu--AlaIleIleGluHisLeuCysAlaSerGluPheAlaLeuArgMetLysIle 213
QY 856 AGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGCAAGACC 915
Db |||||:|:| ||| ||| |||||:|:| ||| ||| |||
214 LysGluValLysLysGluAsnGlyAspLysLysIleVal-----ProLysLysLysLys 231
QY 916 ATTTACAAGCTGAACGGTGTGCCGAAAGGGACCTGAAGAAATCGGTGCTGGCTCAAA 975
Db ||||| :|:| :|:| :|:|:|:| ||||| |||||:|:| |||||:|:| |||||
232 ProLeuLysLeuGlyProIleLysLysLysAspLeuLysLysLeuValLeuTyrLeuLys 251
QY 976 GACAGCTTCAGTGCACCTGTGAGGAGATGACGACATCAACGCGCCCTATCTGTCATG 1035
Db :|:| ||| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
252 AsnGlyAlaAspCysProCysHisGlyLeuAspAsnLeuSerHisPheLeuIleMet 271
QY 1036 GGACAGAAACAGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCAG 1095
Db ||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
272 GlyArgLysValLysSerGlyTyrLeuLeuThrAlaIleHisLysTrpAspLysLysAsn 291
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db :|:|:| ||||| ||| :|:| :|:|:|:|:|:|:|:|:|:|:|:|
292 LysGluPheLysAsnPheMetLysLysMetLysAsnHisGluCys 306

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Search completed: September 1, 2005, 09:41:11  
Job time : 61 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2005, 09:26:23 ; Search time 286 Seconds  
(without alignments)  
5482.261 Million cell updates/sec

Title: US-08-949-904A-1  
Perfect score: 3585  
Sequence: 1 GAATTCGGCCTTCATGGCCT.....AAAAAAGGCGCGCGC 2027

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delopt 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -MODEL=frame\_n2p.model -DEV=xlp  
-Q/cn2\_1/USFT0\_spool\_p/US08949904/runat\_01092005\_102611\_21240/app.query.fasta\_1.2183  
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08949904 @CN\_1\_1\_308 @runat\_01092005\_102611\_21240 -NCRU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1976.5	55.1	377	4 AAG75608	Aag75608 Human col
2	1957.5	54.6	408	2 AAY74087	Aay74087 Human pro
3	1594	44.5	295	2 AAW82588	Aaw82588 Human ATG
4	1594	44.5	295	2 AAW49082	Aaw49082 Homo sapi
5	1594	44.5	295	2 AAY06923	Aay06923 Human sec
6	1594	44.5	295	5 ABG31499	Abg31499 Human sec
7	1594	44.5	295	6 ABU55908	Abu55908 Human pro
8	1594	44.5	295	6 AAE34062	Aae34062 SARP 2 pr
9	1594	44.5	295	6 ABR47455	AbR47455 Breast ca
10	1594	44.5	295	7 ADF77693	Adf77693 Human ful

11	1594	44.5	295	7 ADN40027	Adn40027 Cancer/an
12	1594	44.5	295	8 ADN05090	Adn05090 Antipsoi
13	1594	44.5	295	8 ADR46694	Adr46694 Cancer-ab
14	1590	44.4	295	2 AAY41748	Aay41748 Human PRO
15	1590	44.4	295	3 AAB44304	Aab44304 Human PRO
16	1590	44.4	295	5 ABB84861	Abb84861 Human PRO
17	1590	44.4	295	5 ABB95467	Abb95467 Human arg
18	1590	44.4	295	6 ABO25250	AbO25250 Novel hum
19	1590	44.4	295	6 ABU72256	Abu72256 Novel hum
20	1590	44.4	295	6 ABU84936	Abu84936 Human sec
21	1590	44.4	295	6 ABU61134	Abu61134 Human PRO
22	1590	44.4	295	6 ABU80403	Abu80403 Human sec
23	1590	44.4	295	6 ADA24954	Ada24954 Novel hum
24	1590	44.4	295	6 ABO19705	AbO19705 Novel hum
25	1590	44.4	295	6 ADA12615	Ada12615 Human sec
26	1590	44.4	295	6 ABO19596	AbO19596 Novel hum
27	1590	44.4	295	7 ADB73921	AdB73921 Human PRO
28	1590	44.4	295	7 ADB76637	AdB76637 Human PRO
29	1590	44.4	295	7 ADC44063	AdC44063 Human sec
30	1590	44.4	295	7 ADC61823	AdC61823 Human sec
31	1590	44.4	295	7 ADC63787	AdC63787 Human sec
32	1590	44.4	295	7 ADC66887	AdC66887 Human sec
33	1590	44.4	295	7 ADC69011	AdC69011 Human sec
34	1590	44.4	295	7 ADC63071	AdC63071 Human sec
35	1590	44.4	295	7 ADC68136	AdC68136 Human sec
36	1590	44.4	295	7 ADC41456	AdC41456 Human sec
37	1590	44.4	295	7 ADC67511	AdC67511 Human sec
38	1590	44.4	295	7 ADC62447	AdC62447 Human sec
39	1590	44.4	295	7 ADC42080	AdC42080 Human sec
40	1590	44.4	295	7 ADD10479	AdD10479 Human sec
41	1590	44.4	295	7 ADD11339	AdD11339 Human sec
42	1590	44.4	295	7 ADD37132	AdD37132 Human sec
43	1590	44.4	295	7 ADE49449	AdE49449 Human sec
44	1590	44.4	295	7 ADE35503	AdE35503 Human sec
45	1590	44.4	295	7 ADE16617	AdE16617 Human sec

ALIGNMENTS

RESULT 1  
AAG75608  
ID AAG75608 standard; protein; 377 AA.  
XX AAG75608;  
XX AC AAG75608;  
XX DT 03-SEP-2001 (first entry)  
XX DE Human colon cancer antigen protein SEQ ID NO:6372.  
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
XX KW colorectal carcinoma.  
XX OS Homo sapiens.  
XX PN WO200122920-A2.  
XX PD 05-APR-2001.  
XX PF 28-SEP-2000; 2000WO-US026524.  
XX PR 29-SEP-1999; 99US-0157137P.  
XX PR 03-NOV-1999; 99US-0163280P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX WPI: 2001-235357/24.  
XX DR N-PSDB; AAH35013.  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
XX useful for preventing, diagnosing and/or treating colorectal cancers.

PS Claim 11; Page 7840-7842; 9803pp; English.  
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene therapy  
 CC and vaccine production. N and P may be used in the prevention, diagnosis  
 CC and treatment of diseases associated with inappropriate P expression. For  
 CC example, N and P may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of P by expressing inactive proteins or to  
 CC supplement the patients own production of P. Additionally, N may be used  
 CC to produce the colon cancer-associated PS, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAH37195 to AAH37204 and AAB77789 represent  
 CC sequences used in the exemplification of the present invention. N.B.  
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922  
 XX  
 SQ Sequence 377 AA;

Alignment Scores:  
 Pred. No.: 2,7e-161 Length: 377  
 Score: 1976.50 Matches: 370  
 Percent Similarity: 98.93% Conservative: 0  
 Best Local Similarity: 98.93% Mismatches: 2  
 Query Match: 55.13% Indels: 2  
 DB: 4 Gaps: 1

US-08-949-904A-1 (1-2027) x AAG75608 (1-377)

QY 24 TCATTCTGCTCCCGGGTCGGAGCCCCCGAGGTGCGCGGGCTTCAGCGCTCGC 83  
 DB 5 SerPheCysSerProGlySerGluProProGlyAlaAlaArgGlyLeuAlaAlaProArg 24  
 QY 84 CCGCGCT---CTCCCGGTGTCCTCCCGCCCCCAGCGCGGCTGCGAGCTTTT 140  
 DB 25 Pro-ArgCysProGlyValProLeuLeuArgAlaProAlaAlaGlyCysGlnLeuPh 44  
 QY 141 CCGGGCCCCAGTCCGACCCAGGAGAGAGCGGGCCCGGACAGCTCGAAGTCCGGCC 200  
 DB 44 eGlyAlaProSerArgThrGlnArgArgGluArgAlaArgAspLysLeuGluLeuArgPr 64  
 QY 201 GCTCTGCCCTTCCCGGCTCCGCTCCCTCCCGCTCCCGGCTCCCGGCTCCCGGCTCCG 260  
 DB 64 oProArgProSerProAlaProLeuProLeuProArgGlyArgAlaProThrMetLe 84  
 QY 261 GAGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320  
 DB 84 uGlnGlyProGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 104  
 QY 321 GCGCGGCTCTTCCTCTTGGCCAGCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 380  
 DB 104 aArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCysLePr 124  
 QY 381 CATCCCGGCAACCTGACCTGTCACCGCATCGAATACCAAGATCCAGACATCGCGCTCCCAA 440  
 DB 124 oilePro\*\*\*AsnLeuGlnLeuCysHisGlyLeuGlnAsnMetArgLeuProAs 144  
 QY 441 CTGCTGGCCACGAGACCATGAAGAGTGTGTGAGAGAGCGCGCGCTTGAATCCCGCT 500  
 DB 144 nLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIleProle 164  
 QY 501 GCTCATGAGCAGTCCACCGGACACCAAGATTCTGCTGCTGCTGCTGCTGCTGCTGCT 560  
 DB 164 uValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAlaProVa 184  
 QY 561 CTGCTTCGATGACCTAGACGAGACCATCCAGGCATGCCACTCGCTCTGCTGCTGCTGAA 620  
 DB 184 lCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGlnVally 204

QY 621 CGACGGCTGCGCCCGGCTCATGTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTG 680  
 DB 204 sAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeuGluCy 224  
 QY 681 CGACGGTTTCCCGCCAGGACCAACGACCTTTGTCATCCCTCGCTAGCAGCAGCAGCAGCCT 740  
 DB 224 sAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHisLeule 244  
 QY 741 GCCAGCCACCGAGGAAGCTCCAAAGGTATGTGAAGCTTGAAGCTTGAAGCTTGAAGTGA 800  
 DB 244 uProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAspAs 264  
 QY 801 CAACGACATAATGAAACGCTTTTAAATAATGATTTTGCATGAAATAATAAAGTGAAGGA 860  
 DB 264 pAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysValLysG 284  
 QY 861 GATAACCTTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGAGCAGACCATTTA 920  
 DB 284 uileThrTyrIleAsnArgAspThrLysIleIleuGluThrLysSerLysThrIleTy 304  
 QY 921 CAAGCTGAACGGTGTGTCGAAAGGACCTGAAGAAATCGGTGTGCTGCTGCTCAAGACAG 980  
 DB 304 rLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLysAspSe 324  
 QY 981 CTTGAGTGCACCTGTGAGGAGATCAAGCATCAACGCGCCCTATCTGCTCATGGGACA 1040  
 DB 324 rLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMetGlyG 344  
 QY 1041 GAAACAGGGTGGGAGCTGGTGTGATCCTCGTCAAGCGGTGGCAGAGGGGCGCAGAGAGA 1100  
 DB 344 nLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGlnArgG 364  
 QY 1101 GTTCAAGCGCATCTCCGAGCATCCGAGCATCCGCAAGCTCGAGTGC 1140  
 DB 364 uPheLysArgIleSerArgSerIleArgLysLeuGlnCys 377  
 RESULT 2  
 AA74087  
 ID AA74087 standard; protein; 408 AA.  
 XX AA74087;  
 XX 14-MAR-2000 (first entry)  
 DT Human prostate tumor EST fragment derived protein #274.  
 DE Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;  
 KW treatment.  
 KW Homo sapiens.  
 OS DE19820190-A1.  
 PN 04-NOV-1999.  
 PD 28-APR-1998; 98DE-01020190.  
 PF 28-APR-1998; 98DE-01020190.  
 PR (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;  
 PI WPI; 1999-621386/54.  
 XX N-PSDB; AAZ52948.  
 XX New human nucleic acid sequences from pancreatic tumors, and related  
 PT proteins.  
 XX Claim 23; Page 423; 502pp; German.  
 PS This invention describes novel polypeptides and their encoding nucleic  
 CC acids derived from human pancreatic tumor tissue which have cytostatic



CC activity. The sequences are also useful in producing pharmaceutical  
 CC compositions for treatment of pancreatic tumors. AAY73814-Y74252  
 CC represent protein fragments encoded by the human pancreatic tumor cDNA  
 CC library derived expressed sequence tag (EST) sequences represented in  
 CC AA252858-Z53014  
 XX  
 SQ Sequence 408 AA;

## Alignment Scores:

Pred. No.: 1,21e-159 Length: 408  
 Score: 1957.50 Matches: 372  
 Percent Similarity: 99.20% Conservatives: 0  
 Best Local Similarity: 99.20% Mismatches: 0  
 Query Match: 54.60% Indels: 3  
 DB: 2 Gaps: 1

US-08-949-904A-1 (1-2027) x AAY74087 (1-408)

QY 23 CTCATTCTCTCCCGGGTCCGAGCCCGCGGAGTGGCGGGCTTGCAGCGCTCG 82  
 DB 36 LeuileLeuLeuProArgValGlyAlaProArgSerCysAlaArgAlaCysSerAlaSer 55  
 QY 83 CCGCGCTCTCC---CGGTGTCCTCTCCGCGCCCGCGCGCGCTCCGAGCTTT 139  
 DB 56 ProAlaLeu-SerSerArgCysProAlaSerProArgProSerArgLeuProAlaPh 75  
 QY 140 TCGGGGCCCCGAGTGCACCCAGCAAGAGAGCGGCGCGCGCAAGCTCGAAGCTCCGGC 199  
 DB 75 eArgGlyProGluSerHisProAlaAlaArgAlaGlyProGlyGlnAlaArgThrProAl 95  
 QY 200 CGCTCGCTCTCCCGGGTCCGCTCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 259  
 DB 95 alaSerProProGlySerAlaProSerAlaProSerGlySerArgAlaHisAspAl 115  
 QY 260 TGCAGGGCTCGCTCGCTCGCTCTCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 319  
 DB 115 alaGlyProThrLeuAlaAlaAlaLeuProArgLeuAlaLeuProGlyLeuG 135  
 QY 320 CGCGGGCTCTCTCTCTTTGGCCAGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 379  
 DB 135 yalaArgAlaLeuProLeuTriProAlaArgLeuLeuLeuGlnAlaGln-AlenCysLysP 155  
 QY 380 CATCTCCGGCCAACTGAGCTGTGCGCAGGATCGAATACAGAACATGCGGCTGCCCA 439  
 DB 155 roileProAlaAlaLeuGlnLeuCysHisGlyLeuGlnAlaGlnAlaGlnAlaGlnAla 175  
 QY 440 ACTCTGCGGCCACGAGCAGCAGGAGGCTCTGAGGAGGCTCTGAGGAGGCTCTGAGGAG 499  
 DB 175 enLeuLeuGlyHisGlnThrMetLysGluValLeuGluGlnAlaGlyAlaTriPleProL 195  
 QY 500 TGGTCATGAGCAGTCCACCGGACACCAAGATTCCTGCTCGCTCTCTCTCTCTCTCTCTCT 559  
 DB 195 euValMetLysGlnCysHisProArgThrLysLysPheLeuLeuCysSerLeuPheAlaProV 215  
 QY 560 TCTGCTCGATGACTAGACGAGACATCCAGCCATGCGCTCTGCTGCTGCTGCTGCTGCTG 619  
 DB 215 aLysLeuAspLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGlnValL 235  
 QY 620 AGGACCGCTCGCGCGCTCATGCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCTCGCTCT 679  
 DB 235 yAspArgCysAlaProValMetSerAlaPheGlyPheProTriProAspMetLeuGluC 255  
 QY 680 GCGACCGTTTCCCGGACCAACAGCTTTTGATCCCCCTCGCTAGCAGCGACCACTCC 739  
 DB 255 yAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHisLeuL 275  
 QY 740 TCCAGCCACCGAGGAGCTCCAAAGGTATGTGAAGCTTGCAGCTTGCAGCTTGCAGCTTGC 799  
 DB 275 euProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAspA 295  
 QY 800 ACAACGACATATGAAAGCTTTTGTAAATGATTTCACCTGAAATATAAAGTGAAGG 859  
 DB 295 pAsnAspIleMetGluThrLeuCysLysLysAsnAspPheAlaLeuLysIleLysValLysG 315

QY 860 AGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGACCAAGACCATTT 919  
 DB 315 luileThrTyrlleAsnArgAspThrLysIlelleLeuGluThrLysSerLysThrIleT 335  
 QY 920 ACAAGCTGAACGGTGTGTCGAAAGGGACCTGAGAAATCGGTGCTGGCTCAAGACA 979  
 DB 335 yrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLysAsps 355  
 QY 980 GCTTCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGTCTATGGGAC 1039  
 DB 355 erLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTrpLeuValMetGlyG 375  
 QY 1040 AGAAACAGCGTGGGAGCTGTGTATCACTCGGTGAAGCGGTGGCAGAGGGGCGAGAG 1099  
 DB 375 lnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGlnArgG 395  
 QY 1100 AGTTCAACGGATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140  
 DB 395 luPheLysArgIleSerArgSerIleArgLysLeuGlnCys 408

## RESULT 3

AAW82588  
 ID AAW82588 standard; protein; 295 AA.

AC AAW82588;

XX 01-MAR-1999 (first entry)

XX Human ATG-1622 protein.

XX ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;  
 diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;  
 heart disease; hypertension; kidney disease; insulin resistance;  
 lipodystrophy; diabetes; central nervous system; CNS; gene mapping;  
 linkage analysis.

Homo sapiens.

EP879887-A1.

25-NOV-1998.

14-MAY-1998; 98EP-00302809.

21-MAY-1997; 97US-0047251P.

13-JUN-1997; 97US-00874156.

(SMIK) SMITHKLINE BEECHAM CORP.

Hu E, Zhu Y;

WPI; 1998-596879/51.

N-PSDB; AAV69384.

New human secreted protein ATG-1622 polypeptide and polynucleotide -  
 useful as diagnostic reagents and for prevention and treatment of Central  
 Nervous System diseases and diabetes.

Claim 11; Page 22-23; 28pp; English.

This sequence represents the human ATG-1622 protein which is related to  
 human secreted ligands for 7-transmembrane receptors and similar to  
 murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for  
 diagnosing susceptibility to diseases by detecting mutations in the ATG-  
 1622 gene and can diagnose diseases associated with ATG-1622 imbalance.  
 The polypeptides can be used to screen for agonists and antagonists which  
 can be used in treatment to activate or inhibit ATG-1622 activity. The  
 ATG-1622 polypeptide can be administered directly or as a vaccine to  
 inoculate against disease. Diseases which can be diagnosed, prevented or  
 treated by the ATG-1622 polypeptide or polynucleotides include heart  
 disease, hypertension, kidney diseases, obesity, insulin resistance,  
 lipodystrophy, diabetes and central nervous system (CNS) diseases. The







Db	1	MetLeuGlnGlyProGlySerLeuLeuLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly	20
QY	316	TCGGCGCGGGCTCTCTCTCTTTGGCCAGCCGACTTCTCTTACAAGCGCGACATTCG	375
Db	21	SerAlaArgGlyLeuPheLeuPheGlyGlnProAapPheSerTyrLysArgSerAnCys	40
QY	376	AGCCCATCCCGCCCACTGAGCTGTCCAGCGCATCGAATACAGAACATCGCGCTG	435
Db	41	LysProIleProAlaAenLeuGlnLeuCysHisGlyIleGluTyrGlnAenMetArgLeu	60
QY	436	CCCAACCTCTCGTGGCCAGACCATGAAGAGGTGTGGAGCAGCGCGCTTGGATC	495
Db	61	ProaenLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaIalatrIle	80
QY	496	CCGCTGTGTCATGAAGCAGTGCACCCGCGACCAAGAGTTCCTGTCTCGCTCTTCGCC	555
Db	81	ProLeuValMetLysGlnCysHisProAapThrLysLysPheLysCysSerLeuPheAla	100
QY	556	CCGCTGTGCTGATGACCTAGACGAGACCATCCAGCCATCGCATCTCGCTCTCGTGAG	615
Db	101	ProValCysLeuAapLeuAapGluThrIleGlnProCysHisSerLeuCysValGln	120
QY	616	GTGAAGGACCGCTGCGCCGCTGATGCTCGCTTCCGCTTCCCTGCGCCGACATGCTT	675
Db	121	VallysAapArgCysAlaProValMetSerAlaPheGlyPheProTrpProAapMetLeu	140
QY	676	GAGTGGCAGCGTTTCCCCAGACACGACCTTTGTCATCCCCCTCGTAGCAGCACCAC	735
Db	141	GluCysAapArgPheProGlnAapAenAapLeuCysIleProLeuAlaSerSerAphis	160
QY	736	CTCTGCGCAGCCAGCAGAGCTCAAGAGTATGTGAAGCTGCAAAATATAAATGAT	795
Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAenLysAenAap	180
QY	796	GATGACACGACATATGATGACGCTTGTAAATGATTTTGCCTGAAATRAAGTG	855
Db	181	AapAapAenAapIleMetGluThrLeuCysLysAenAapPheAlaLeuLysIleLysVal	200
QY	856	AAGGAGATAACCTACATCAACGAGATACCAAAATCATCTCGAGACCAAGACGACC	915
Db	201	LysGluIleThrTyrIleAenAapThrLysIleIleLeuGluThrLysSerLysThr	220
QY	916	ATTACAGCTGAAGGTGTGTCGAAGGAGCCTGAGAAATCGGTGCTGTGCTCAAA	975
Db	221	IleTyrLysLeuAenGlyValSerGluArgAapLeuLysLysSerValLeuTrpLeuLys	240
QY	976	GACAGCTTGCAGTCACCTGTGAGGAGATGACGACATCAACGCGCCCTATCTGCTCATG	1035
Db	241	AapSerLeuGlnCysThrCysGluMetAenAapIleAenAlaProTyrLeuValMet	260
QY	1036	GCACAGAAACAGGTGGGAGCTGTGATCACCTCGGTGAAGCGGTGGCAGAGGGCAG	1095
Db	261	GlyGlnLysGlnGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280
QY	1096	AGAGAGTTCAAGCGCATCTCCGCGAGCATCCCAAGTGCAGTGC	1140
Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295
RESULT 7			
ID	ABU55908	standard; protein; 295 AA.	
XX	AC	ABU55908;	
XX	DT	25-MAR-2003 (first entry)	
XX	DE	Human protein SARP 2.	
KW	Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;		
KW	ligand; Parkinson's disease; Huntington's disease; motor neuron disease;		
KW	heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;		
KW	acquired immunodeficiency syndrome.		
XX			

OS Homo sapiens.

XX WO200277204-A2.

XX 03-OCT-2002.

XX 25-MAR-2002; 2002WO-GB001195.

XX 23-MAR-2001; 2001GB-00007296.

PR 23-MAR-2001; 2001GB-00007299.

PR 17-APR-2001; 2001GB-00009346.

XX (AXOR-) AXORDIA LTD.

XX Andrews P, Walsh J, Gokhale P;

XX WPI: 2003-092852/08.

DR N-PSDB; ABX75335.

XX Modulating the differentiation of embryonic stem cells by providing

PT ligands which bind receptors in the Notch and Wnt pathways, useful for

PT treating diseases such as Parkinson's, Huntington's, heart disease,

PT diabetes and AIDS.

XX Disclosure; Fig 82; 121pp; English.

XX The invention relates to modulating the differentiation of an embryonic

XX stem cell, comprising: (a) providing a culture of embryonic stem cells;

XX (b) providing at least one ligand or its active binding fragment, capable

XX of binding its cognate receptor polypeptide expressed by the embryonic

XX stem cell; and (c) forming a culture comprising embryonic stem cells and the

XX ligand; and (d) growing the cell culture. Also included are: (i)

XX Modulating the differentiation of embryonic stem cells, comprising: (a)

XX providing a cell transfected with a nucleic acid molecule selected from:

XX (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic

XX acid molecule that hybridises to the nucleic acid in (i), and which

XX encodes a ligand capable of modulating embryonic stem cell

XX differentiation, or capable of binding a Wnt receptor; or (iii) nucleic

XX acid molecules which are degenerate as a result of the genetic code to

XX the sequences of (i) or (ii); (b) forming a culture comprising the cell

XX identified in (a) with an embryonic stem cell; and (c) growing the

XX culture for the maintenance and/or differentiation of the embryonic stem

XX cell; (2) inhibiting the differentiation of embryonic stem cells,

XX comprising: (a) providing at least one polypeptide or its active

XX fragment, that are inhibitors of the Wnt signalling pathway; (b) forming

XX a culture comprising the cell identified in (a) with an embryonic stem

XX cell; and (c) growing the culture for the maintenance of embryonic stem

XX cells in an undifferentiated state; or (3) inhibiting the differentiation

XX of embryonic stem cells, comprising: (a) providing a cell transfected

XX with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt

XX inhibitory polypeptide; (ii) a molecule which hybridises to the molecule

XX of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;

XX and (iii) nucleic acid molecules which are degenerate as a result of the

XX genetic code to the sequences of (i) or (ii); (b) forming a culture

XX comprising the cell identified in (a) with an embryonic stem cell; and

XX (c) growing the culture for the maintenance of embryonic stem cells in an

XX undifferentiated state; and (4) A cell, therapeutic cell or cell culture

XX obtainable by any of the methods cited above. The therapeutic cell of the

XX present invention is useful in the treatment of an animal, preferably a

XX human, comprising administering a cell composition comprising embryonic

XX stem cells which have been induced to differentiate into at least one

XX cell-type. The cell is also useful for the manufacture of a composition

XX for use in treatment of diseases such as Parkinson's disease,

XX Huntington's disease, motor neuron disease, heart disease, diabetes,

XX liver disease (e.g. cirrhosis), renal disease and AIDS (acquired

XX immunodeficiency syndrome). The present sequence is represents a Wnt or

XX Notch pathway protein (i.e. a ligand for the method of the invention)

XX

SQ Sequence 295 AA;

Alignment Scores:

Pred. No.:

Score:

2.44e-128 Length:

1594.00 Matches:

295

295





Qy	736	CTCTCCGAGCCACCGAGGAAGCTCCAAAGGTATGTGAAGCCTCGAAAAATAAAAAATGAT	795
Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp	180
Qy	796	GATCACAAACGACATAAATGGAAACGCTTTGTAATAATGATTTTGACACTGAAATAATAAAGTG	855
Db	181	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200
Qy	856	AAGGAGATAACTTACATCAACCGAGATACCAAAAATCATCTCGAGAGACCAAGACGACGACC	915
Db	201	LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr	220
Qy	916	ATTTACAAGCTGAACCGGTGTCTCGAAAGGGAAGCTCGAAGAAATCGGTGCTGTGGCTCAAA	975
Db	221	IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240
Qy	976	GACAGCTTGAGTGCACCTGTGAGGAGATGAACGACATCAACGGCGCCTATCTGGTCATG	1035
Db	241	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlLeuValMet	260
Qy	1036	GGACAGAAAAACGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAG	1095
Db	261	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280
Qy	1096	AGAGATTCAAGCGGCATCTCTCCGCGAGCATCCGCAAGCTGCAGTGC	1140
Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295

**RESULT 10**

ADF77693

ID ADF77693 standard; protein; 295 AA.

XX

AC ADF77693;

XX

DT	26-FEB-2004	(first entry)
XX		
DE		Human full length Frazzled family protein SDF-5.
XX		
KW		Human; Frazzled family protein; SDF-5; pancreatic gene; chondrocyte differentiation; cartilage tissue formation; tissue repair; pancreatic tissue repair; cartilage disorders; osteoarthritis; rheumatoid arthritis; articular cartilage defect; nutritional source; nutritional supplement; immune deficiency; infection; HIV infection; hepatitis; cancer; diabetes; inflammation; asthma; neurological disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease.

05 Homo sapiens.

XX  
: error? for amount

FH	Key	Location/Qualifiers
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FT	Peptide	1. .20

FT	/note= "Signal peptide"
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2	
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100	

FT	Region	18. .295
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FT /note= "Claimed in claim

FT	Region	19.	.295
FT	Region	19.	.295

[illegible]

Region	FT
20.295	

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FT      /note= "Claimed in claim
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PT	protein	21. .295	/label =	Methionine	one
EM					

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F1 /label= Mature_SDF_5
E1 /not= "Claimed in claim"

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FT	Region	22	205
FI		/note= "Claimed in claim	

FI region  
22. .295  
/note- "Claimed in claim

FI	Region	FT	23	295
/note="Claimed in claim				

ET	region	23. .233	/note= "Claimed in claim
ET			

FT Region 24, .295

FT /note= "Claimed in claim

FT	Region	25. .295
----	--------	----------

FT /note= "Claimed in claim

PN US2003175855-A1.

XX

PD

XX

PF	15-OCT-1997;	97US-00949904.	
XX			
PR	06-FEB-1997;	97US-00796153.	
PR	08-MAY-1997;	97US-00848439.	
XX			
PA	(LAVA/) LAVALLIE E R.		
PA	(RACI/) RACIE L A.		
XX			
PI	Lavallie ER, Racie LA;		
XX			
DR	WPI, 2003-899533/82.		
DR	N-PSDB; ADF77692.		
XX			
PT	New human SDF-5 DNA, useful for inducing formation, growth,		
PT	differentiation, proliferation or maintenance of chondrocytes or		
PT	cartilage tissues, or as nutritional sources or supplements.		
XX			
PS	Claim 18; SEQ ID NO 2; 24pp; English.		
XX			
CC	The invention relates to an isolated DNA sequence encoding mature or full		
CC	length human SDF-5 (a frazzled family member) or its defined fragments,		
CC	or which hybridises to it under stringent hybridisation conditions and,		
CC	encodes a protein that exhibits Frazzled activity. Also included are a		
CC	vector comprising the above DNA molecule in operative association with an		
CC	expression control sequence, a host cell transformed with the vector, a		
CC	method for producing purified human SDF-5 protein, a purified human SDF-5		
CC	polypeptide, a composition comprising a therapeutic amount of at least		
CC	one human SDF-5 polypeptide cited above, a method for altering the		
CC	regulation of pancreatic genes in a patient (comprising administering to		
CC	the patient an amount of the composition cited above), antibodies to a		
CC	purified human SDF-5 protein and a method for increasing the		
CC	differentiation of cells into chondrocytes, comprising applying a		
CC	composition comprising BMP-2 (Bone morphogenetic protein-2) and SDF-5.		
CC	The DNA and protein are useful in regulating the binding of Wnt (wingnut)		
CC	genes to their receptor or in inducing formation, growth,		
CC	differentiation, proliferation and/or maintenance of chondrocytes and/or		
CC	cartilage tissue, and for other tissue repair, such as pancreatic tissue		
CC	repair. These may be used in the treatment of cartilage disorders, such		
CC	as osteoarthritis, rheumatoid arthritis or articular cartilage defects.		
CC	These may also be used for augmenting the activity of other tissue		
CC	regenerating and differentiation factors. In addition, the protein and		
CC	DNA are used as nutritional sources or supplements and in treating		
CC	various immune deficiencies and disorders (e.g. infections, HIV,		
CC	hepatitis, cancer, diabetes, inflammation or asthma) or neurological		
CC	disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's		
CC	disease). The present sequence represents full length human SDF-5.		
XX			
SQ	Sequence 295 AA;		
	Alignment Scores:		
	Pred. No.: 2,44e-128 Length: 295		
	Score: 1594.00 Matches: 295		
	Percent Similarity: 100.00% Conservative: 0		
	Best Local Similarity: 100.00% Mismatches: 0		
	Query Match: 44.46% Indels: 0		
	DB: 7 Gaps: 0		
US-08-949-904A-1 (1-2027) x ADF77693 (1-295)			
Qy	256 ATGCTGCAGGGCCCTGGCTGCTGCTGCTCTTCCTTCGCTCGCATGCTGCTGGCG 315		
Db	1 MetLeuGlnGlyProGlySerLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20		
Qy	316 TCGCGCGCGGGCTTCCTCTTTGGCCAGCCGACCTTCCTACAAGCGCAGCAATTGC 375		
Db	21 SerAlaargGlyLeuPheLeuPheGlyGlnProaspPheSerTyrLysArgSerAsnCys 40		
Qy	376 AAGCCCATCCGCGGCAACCTCGAGCTGTGCCACGCGCATCGCAATACAGAAATCGCGGTG 435		
Db	41 LysProIleProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrGlnAsnMetArgLeu 60		
Qy	436 CCCAACTGCTGGGCCACGAGACCATGAAGAGGTGCTGGAGACGAGCCGCGCTTGATC 495		



Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80  
QY 496 CCGCTGGTCATGAAGCAGTGCACCCGAGCACCAGAAAGTCTCTGCTCGCTCTTCGCC 555  
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysPheLysCysSerLeuPheAla 100  
QY 556 CCGCTCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCTGCGTGCAG 615  
Db 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120  
QY 616 GTGAGGACCGCTGGCCCGCTGATGCTCGGCTTCGGCTTCCCTGGCCGACATGCTT 675  
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140  
QY 676 GAGTGCAGCCGTTTCCCCAGACACGACCTTTGTCATCCCTCGCTAGCAGCAGCACAC 735  
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160  
QY 736 CTCCTGCCAGCCACCGAGAAAGCTCAAAAGGTATGTGAAGCTGCAAAATATAAATGAT 795  
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180  
QY 796 GATGACACGACATATGATGAAACGCTTGTAAATGATTTGCCACTGAAATAAAGTG 855  
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200  
QY 856 AAGGAGATAACCTACATCAACGAGATACCAAAATCATCTCGAGACCAAGCAAGACC 915  
Db 201 LysGluIleThrTyrlleAsnArgAspThrLysIlelleLeuGluThrLysSerLysThr 220  
QY 916 ATTTCAAGCTGAACGGTGTGTCGAAAGGACCTGAAAGAAATCGGTGCTGGCTCAAA 975  
Db 221 IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240  
QY 976 GACACTTGCATGACCTGTCAGAGATGAACGACATCAACGCCCTATCTGTCATG 1035  
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260  
QY 1036 GCACAGAACAGGGTGGGAGCTGGTGATCACCTCGGTGAACGGTGGCAGAAAGGGCAG 1095  
Db 261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280  
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140  
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295  
RESULT 11  
ADN40027  
ID ADN40027 standard; protein; 295 AA.  
XX AC ADN40027;  
XX DT 17-JUN-2004 (first entry)  
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.  
XX KW Human; differential expression; cancer; angiogenic disorder;  
XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
XX KW inflammatory disease; autoimmune disease;  
XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
XX KW detection; diagnosis; prognosis; drug screening; drug targeting;  
XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
XX KW vulnery; gene therapy; vaccine.  
XX OS Homo sapiens.  
XX PN WO2003042661-A2.  
XX PD 22-MAY-2003.  
XX PF 13-NOV-2002; 2002WO-US036810.  
XX PR 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
PA Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX WPI; 2003-468649/44.  
DR N-PSDB; ADN39810.  
XX  
PT Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
PS Claim 12; SEQ ID NO C397; 1385pp; English.  
XX  
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
SQ Sequence 295 AA;  
Alignment Scores:  
Pred. No.: 2,44e-128 Length: 295  
Score: 1594.00 Matches: 295  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 44.46% Indels: 0  
DB: 7 Gaps: 0  
US-08-949-904A-1 (1-2027) x ADN40027 (1-295)  
QY 256 ATGCTGCAGGGCCCTGGCTCGCTGCTGCTCTCTCTCTCGCTCGCACTGCTGCTGGC 315  
Db 1 MetLeuGlnGlyProGlySerLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20  
QY 316 TCGCGCGCGCGGCTCTTCTCTCTTTGGCCAGCCCGCACTTCTCTCTACAGCGCAGCAATTGC 375  
Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCys 40  
QY 376 AAGCCCATCCCGGCCAACCTGACGTGTGCCACGGCATCGAATACCAAGAAATCGGCTG 435  
Db 41 LysProIleProAlaAsnLeuGlnLeuCysHisGlylleGluTyrGlnAsnMetArgLeu 60

QY	436	CCCAACCTGCTGGCCACGAGACCATGAGGAGGTGCTGGAGCGCGCGCTTGGATC	495	PI	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;		
Db	61	ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle	80	XX	Wu TD;		
QY	496	CCGCTGGTCATGAAGCAGTGCACCGGACACCAAGAGTTCTGTGCTGCTCTTCGCC	555	DR	WPI; 2004-305105/28.		
Db	81	ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla	100	XX	N-PSDB; ADN05089.		
QY	556	CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCGTGCAG	615	PT	New PRO nucleic acid or polypeptide, useful for preparing a		
Db	101	ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln	120	PT	pharmaceutical composition for diagnosing or treating psoriasis in a		
QY	616	GTGAAGGACCGTGGCCCGCTCATGTCGCTTCGGCTTCCTGCTGGCCGACATGCTT	675	XX	mammal.		
Db	121	VallysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu	140	PS	Claim 9; SEQ ID NO 1484; 3069pp; English.		
QY	676	GAGTGCAGCGTTTCCCCCAGACCAACGACCTTTGCATCCCCCTCGTAGCAGCACAC	735	XX	The invention relates to novel polynucleotide and polypeptides for		
Db	141	GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis	160	CC	treating psoriasis or a sequence having at least 80% identity to the		
QY	736	CTCCTGCCAGCCAGGAGAGCTCCAAAGGTATGTGAAGCTTGAAGCTGCAAAATGAT	795	CC	above sequences. The nucleic acid is useful for preparing a composition		
Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp	180	CC	for diagnosing or treating psoriasis in a mammal. This sequence		
QY	796	GATGACACGACATAATGGAACGCTTGTGTAATAATGATTTTGGCACTGAAAATGATG	855	CC	corresponds to one of the polypeptides of the invention.		
Db	181	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200	XX			
QY	856	AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGACACC	915	SQ	Sequence 295 AA;		
Db	201	LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr	220	Alignment Scores:			
QY	916	ATTTCACAGCTGAACGGTGTGTCGAAAGGACCTTGAAGAAATCGGTGCTGGCTCAAA	975	Pred. No.:	2.44e-128		
Db	221	IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240	Score:	1594.00		
QY	976	GACAGCTTCGAGTCACCTGTCGAGGATGAACGACATCAACGCGCCCTATCTGGTCATG	1035	Percent Similarity:	100.00%		
Db	241	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlLeuValMet	260	Best Local Similarity:	100.00%		
QY	1036	GCACAGAAACAGGGTGGGAGCTGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAG	1095	Query Match:	44.46%		
Db	261	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280	Indels:	0		
QY	1096	AGAGAGTTCAAGGGCATCTCCCGAGCATCCGCGAGCATCCGCAAGCTGCGATGC	1140	Gaps:	0		
Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295	US-08-949-904A-1 (1-2027) x ADN05090 (1-295)			
QY	256	ATGCTGACGAGCCCTGGCTCGCTGCTGCTCTTCTCTCGCTCGCTGCTGCTGCTGCGC	315	QY	256	ATGCTGACGAGCCCTGGCTCGCTGCTGCTCTTCTCTCGCTCGCTGCTGCTGCTGCGC	315
Db	1	MetLeuGlnGlyProGlySerLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly	20	Db	1	MetLeuGlnGlyProGlySerLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly	20
QY	316	TCGCGCGCGGGCTTCTCTCTTTGGCAGCCGACTTCTCTCAAGCGCAGCAATGCG	375	QY	316	TCGCGCGCGGGCTTCTCTCTTTGGCAGCCGACTTCTCTCAAGCGCAGCAATGCG	375
Db	21	SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrlLysArgSerAsnCys	40	Db	21	SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrlLysArgSerAsnCys	40
QY	376	AAGCCCATCCCGGCCAACCTGCAGCTGTGCCAGCATCGAATACCGAAGCATCGGCTG	435	QY	376	AAGCCCATCCCGGCCAACCTGCAGCTGTGCCAGCATCGAATACCGAAGCATCGGCTG	435
Db	41	LysProIleProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrlGlnAsnMetArgLeu	60	Db	41	LysProIleProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrlGlnAsnMetArgLeu	60
QY	436	CCCAACCTGCTGGGCCACGAGACCATGAAGAGAGTGTGGAGCAGCGCGCTTGGATC	495	QY	436	CCCAACCTGCTGGGCCACGAGACCATGAAGAGAGTGTGGAGCAGCGCGCTTGGATC	495
Db	61	ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle	80	Db	61	ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle	80
QY	496	CCGCTGGTCATGAAGCAGTGCACCGGACACCAAGAGTTCTCTGCTCGCTCTTCGCC	555	QY	496	CCGCTGGTCATGAAGCAGTGCACCGGACACCAAGAGTTCTCTGCTCGCTCTTCGCC	555
Db	81	ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla	100	Db	81	ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla	100
QY	556	CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCGTGCAG	615	QY	556	CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCGTGCAG	615
Db	101	ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln	120	Db	101	ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln	120
QY	616	GTGAAGGACCGTGGCCCGCTCATGTCGCTTCGGCTTCCTGCTGGCCGACATGCTT	675	QY	616	GTGAAGGACCGTGGCCCGCTCATGTCGCTTCGGCTTCCTGCTGGCCGACATGCTT	675
Db	121	VallysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu	140	Db	121	VallysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu	140
QY	676	GAGTGCAGCGTTTCCCCCAGGACCAACGACCTTTGCATCCCCCTCGTAGCAGCACAC	735	QY	676	GAGTGCAGCGTTTCCCCCAGGACCAACGACCTTTGCATCCCCCTCGTAGCAGCACAC	735
Db	141	GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis	160	Db	141	GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis	160
QY	736	CTCCTGCCAGCCAGGAGAGCTCCAAAGGTATGTGAAGCTTGAAGCTGCAAAATGAT	795	QY	736	CTCCTGCCAGCCAGGAGAGCTCCAAAGGTATGTGAAGCTTGAAGCTGCAAAATGAT	795
Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp	180	Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp	180
QY	796	GATGACACGACATAATGGAACGCTTGTGTAATAATGATTTTGGCACTGAAAATGATG	855	QY	796	GATGACACGACATAATGGAACGCTTGTGTAATAATGATTTTGGCACTGAAAATGATG	855
Db	181	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200	Db	181	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200
QY	856	AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGACACC	915	QY	856	AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGACACC	915
Db	201	LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr	220	Db	201	LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr	220
QY	916	ATTTCACAGCTGAACGGTGTGTCGAAAGGACCTTGAAGAAATCGGTGCTGGCTCAAA	975	QY	916	ATTTCACAGCTGAACGGTGTGTCGAAAGGACCTTGAAGAAATCGGTGCTGGCTCAAA	975
Db	221	IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240	Db	221	IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240
QY	976	GACAGCTTCGAGTCACCTGTCGAGGATGAACGACATCAACGCGCCCTATCTGGTCATG	1035	QY	976	GACAGCTTCGAGTCACCTGTCGAGGATGAACGACATCAACGCGCCCTATCTGGTCATG	1035
Db	241	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlLeuValMet	260	Db	241	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlLeuValMet	260
QY	1036	GCACAGAAACAGGGTGGGAGCTGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAG	1095	QY	1036	GCACAGAAACAGGGTGGGAGCTGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAG	1095
Db	261	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280	Db	261	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280
QY	1096	AGAGAGTTCAAGGGCATCTCCCGAGCATCCGCGAGCATCCGCAAGCTGCGATGC	1140	QY	1096	AGAGAGTTCAAGGGCATCTCCCGAGCATCCGCGAGCATCCGCAAGCTGCGATGC	1140
Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295	Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295
QY	ADN05090	standard; protein; 295 AA.		RESULT 12			
XX	ADN05090;			ID	ADN05090		
XX	ADN05090;			AC	ADN05090;		
XX	ADN05090;			AC	ADN05090;		
DT	01-JUL-2004 (first entry)			DT	01-JUL-2004 (first entry)		
DE	Antipsoriatic protein sequence #724.			DE	Antipsoriatic protein sequence #724.		
XX	antipsoriatic; gene therapy; psoriasis; diagnosis.			XX	antipsoriatic; gene therapy; psoriasis; diagnosis.		
KW	antipsoriatic; gene therapy; psoriasis; diagnosis.			KW	antipsoriatic; gene therapy; psoriasis; diagnosis.		
OS	Homo sapiens.			OS	Homo sapiens.		
XX	WO2004028479-A2.			XX	WO2004028479-A2.		
PN	08-APR-2004.			PN	08-APR-2004.		
PD	25-SEP-2003; 2003WO-US030907.			PD	25-SEP-2003; 2003WO-US030907.		
PF	25-SEP-2002; 2002US-0414006P.			PF	25-SEP-2002; 2002US-0414006P.		
XX	(GETH ) GENENTECH INC.			XX	(GETH ) GENENTECH INC.		
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Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80  
QY 496 CCGCTGGTCATGAAGCAGTGCACCCCGAGCACCAAGATTCCTGTGCTCGCTCTTCGCG 555  
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysPheLeuLysSerLeuPheAla 100  
QY 556 CCGCTGCTGATGACCTAGACGAGACATCCAGCCATGCCATCGCTCTGCGTGCAG 615  
Db 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120  
QY 616 GTGAGGACCGCTGCGCCCGCTGATGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 675  
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140  
QY 676 GAGTGGACCGTTTCCCGAGACACGACCTTTGTCATCCCTCGCTAGCAGCACAC 735  
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160  
QY 736 CTCCTGCCAGCCAGGAGAGCTCCAAAGGTATGTGAAGCTGCAAAATATAAATATGAT 795  
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180  
QY 796 GATGACACGACATATGAAACGCTTTCTTAAATGATTTTGCATCGATGAAATAAAGTG 855  
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200  
QY 856 AAGGAGATACCTACATCAACGAGATACCAAAATCATCTCGAGACCAAGAGCAGACC 915  
Db 201 LysGluIleThrTyrlleAsnArgAspThrLysIleIleGluThrLysSerLysThr 220  
QY 916 ATTTCAAGCTGAACGGTGTGTCGAAAGCGACCTGAAGAAATCGGTGCTGTGCTCAA 975  
Db 221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240  
QY 976 GACAGCTTCAGTGCACCTGTGAGGAGATGAAGACATCAACGCGCCCTATCTGTGTCATG 1035  
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260  
QY 1036 CGACAGAAACAGGGTGGGAGCTGTGTATCACCTCGTGAAGCGGTGGCAGAGGGCAG 1095  
Db 261 GlyGlnLysGlnGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280  
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCATGC 1140  
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295  
RESULT 15  
ID AAB44304 standard; protein; 295 AA.  
AC AAB44304;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human PRO697 (UNQ361) protein sequence SEQ ID NO:415.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;  
KW expressed sequence tag; detection; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200053756-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 18-FEB-2000; 2000WO-US004341.  
XX  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 29-MAR-1999; 99US-0126773P.  
PR 21-APR-1999; 99US-0130232P.  
PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
DR WPI: 2000-611443/58.  
DR N-PSDB; AAC78560.  
XX  
PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.  
XX  
PS Claim 12; Fig 167; 636pp; English.  
XX  
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
SQ Sequence 295 AA;  
Alignment Scores:  
Pred. No.: 5,4e-128 Length: 295  
Score: 1590.00 Matches: 294  
Percent Similarity: 99.66% Conservative: 0  
Best Local Similarity: 99.66% Mismatches: 1  
Query Match: 44.35% Indels: 0  
DB: 3 Gaps: 0  
US-08-949-904A-1 (1-2027) x AAB44304 (1-295)  
QY 256 ATGCTGCAGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315  
Db 1 MetLeuGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20  
QY 316 TCGCGCGCGGGCTCTTCTCTTTGGCCAGCCCGCTTCTCTTCAAGCGCAGCAATTCG 375  
Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCys 40  
QY 376 AAGCCCATCCCGCCCAACCTGCAGCTGCGCAGCGCATCGAATACCGAAGATCGGCTG 435  
Db 41 LysProIleProValAsnLeuGlnCysHisGlyIleGluTyrGlnAsnMetArgLeu 60  
QY 436 CCCAACCTGCTGGGCCCACGAGACCATGAAGAGAGTGTGGAGCAGCGCGCTTGGATC 495  
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80  
QY 496 CCGCTGGTTCATGAAGCAGTGCACCCGAGCACCAAGATTCCTGTGCTCGCTCTTCGCG 555  
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100

QY 556 CCGCTCTGCCTCGATGACCTAGACGAGACCATCCAGCATGCCACTCGCTCTGCCTGCAG 615  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120  
QY 616 GTGAGGACCGCTGCGCCCGGTCATGTCGGCTTCGGCTTCCTGGCCCGACATGCTT 675  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140  
QY 676 GAGTGGACCGTTTCCCCAGGACAAACGACCTTTGTCATCCCTCGCTAGCAGCCACAC 735  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160  
QY 736 CTCCTGCCAGCCACCGAGAGAGCTCCAAAGGTATGTGAAGCCTGCAGAAATATAAATGAT 795  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180  
QY 796 GATGACAAACGACATAATGAAACGCTTTGTAAAAATGATTTGCACTGAAAAATAAAAGTG 855  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200  
QY 856 AGGAGATACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGACCAAGACC 915  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
201 LysGluIleThrTyriLeAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220  
QY 916 ATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAAATCGGTGCTGTGGCTCAA 975  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240  
QY 976 GACAGCTTCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGGTTCATG 1035  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260  
QY 1036 GGACAGAAAACAGGTGGGAGCTGTGTATCATCTCGTGAACGGTGGCAGAAAGGGGCAG 1095  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280  
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 1, 2005, 09:51:02 ; Search time 118.518 Seconds  
(without alignments)  
1274.608 Million cell updates/sec

Title: US-08-949-904A-2

Perfect score: 1594

Sequence: 1 MLQPGSLLLLFLASHCCLG.....WKGQREPKRISRIRKLQC 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	2 Q9HAP5	Q9HAP5 homo sapien
2	1590	99.7	295	2 Q9GHF1	Q9GHF1 homo sapien
3	1560	97.9	295	2 O08862	O08862 mus musculus
4	1557	97.7	295	2 O35297	O35297 mus musculus
5	1557	97.7	295	2 P97299	P97299 mus musculus
6	1550.5	97.3	294	2 Q863H1	Q863H1 canis famli
7	1515	95.0	283	2 Q9BG86	Q9BG86 oryctolagus
8	1318	82.7	295	2 Q6P8B8	Q6P8B8 xenopus tro
9	1299	81.5	292	2 Q9IA96	Q9IA96 gallus gall
10	1283	80.5	298	2 Q72XM6	Q72XM6 xenopus lae
11	1116	70.0	206	2 O14778	O14778 homo sapien
12	667.5	41.9	310	2 Q6YNR8	Q6YNR8 brachydanio
13	631	39.6	314	2 Q8K269	Q8K269 mus musculus
14	627	39.3	306	2 Q6GZK1	Q6GZK1 oryzias lat
15	627	39.3	314	2 Q9WU66	Q9WU66 mus musculus
16	619	38.8	315	2 Q9XSC1	Q9XSC1 bos taurus
17	618.5	38.8	296	2 Q7T2K9	Q7T2K9 brachydanio
18	618.5	38.8	315	2 Q640J3	Q640J3 xenopus lae
19	614.5	38.6	317	2 O14780	O14780 homo sapien
20	613.5	38.5	315	2 Q8AWG4	Q8AWG4 xenopus lae
21	611.5	38.4	315	2 Q6GL50	Q6GL50 xenopus tro
22	604	37.9	313	2 O00546	O00546 homo sapien
23	602	37.8	314	2 O14779	O14779 homo sapien
24	602	37.8	314	2 Q8N474	Q8N474 homo sapien
25	596.5	37.4	308	2 O19116	O19116 bos taurus
26	594	37.3	314	2 Q8R1J4	Q8R1J4 mus musculus
27	592	37.1	314	2 O08861	O08861 mus musculus
28	591.5	37.1	272	2 Q8C4U3	Q8C4U3 mus musculus
29	583.5	36.6	311	2 Q9YI24	Q9YI24 xenopus lae
30	573.5	36.0	314	2 Q9DEQ4	Q9DEQ4 gallus gall
31	501	31.4	307	2 O42397	O42397 gallus gall

RESULT 1

ID	Q9HAP5	PRELIMINARY;	PRT;	295	AA.
AC	Q9HAP5				
DT	01-MAR-2001	(Tremblrel. 16, Created)			
DT	01-MAR-2001	(Tremblrel. 16, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	Pancreas tumor-related protein.				
GN	Name=PKSG12;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NC	NCBI_TaxID=9606;				
RN	[1] SEQUENCE FROM N.A.				
RA	Wang Y.-G.;				
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL;	AF311912;	AAG24923.1;	-;	
DR	PIR;	JE0174;	JE0174.	-;	
DR	HSSP;	O61091;	I1JY.	-;	
DR	Genew;	HGNC:10777;	SFRP2.	-;	
DR	GO;	GO:0016020;	C:membrane;	IEA.	
DR	GO;	GO:0004888;	F:transmembrane receptor activity;	IEA.	
DR	GO;	GO:0007275;	P:development;	IEA.	
DR	InterPro;	IPR000024;	Fz domain.		
DR	InterPro;	IPR001134;	Netrin-C.		
DR	InterPro;	IPR008993;	TIMP_like.		
DR	Pfam;	PF01392;	Fz; 1.		
DR	Pfam;	PF01759;	NTR; 1.		
DR	SMART;	SM00643;	C345C; 1.		
DR	SMART;	SM00063;	FRI; 1.		
DR	PROSITE;	PS0038;	FZ; 1.		
DR	PROSITE;	PS0189;	NTR; 1.		
DR	SEQUENCE	295	AA;	33490	MW; 975979715418FBC4 CRC64;
Query Match 100.0%; Score 1594; DB 2; Length 295;					
Best Local Similarity 100.0%; Pred.No. 5.7e-118;					
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLQPGSLLLLFLASHCCLGSARGLFLFGQDPFSYKRSNCKP	IPANLQCHGIEYQNRL	60	
Db	1	MLQPGSLLLLFLASHCCLGSARGLFLFGQDPFSYKRSNCKP	IPANLQCHGIEYQNRL	60	
Qy	61	PNLLGHETMKVLEQAGAWPLVMKQCHPDTKFKLCSLFA	PVCUDDDETTPCHSLCVQ	120	
Db	61	PNLLGHETMKVLEQAGAWPLVMKQCHPDTKFKLCSLFA	PVCUDDDETTPCHSLCVQ	120	
Qy	121	VKDCAPVMSAFGPPWPDMLCDRFPQNDLCIFLASSDHL	LPPATEBAPKVEACKNKND	180	
Db	121	VKDCAPVMSAFGPPWPDMLCDRFPQNDLCIFLASSDHL	LPPATEBAPKVEACKNKND	180	
Qy	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSK	ITYKLVNGVSRDLKKSVLWK	240	
Db	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSK	ITYKLVNGVSRDLKKSVLWK	240	

QY 241 DSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWKQKQREFKRSIRKLCQ 295  
 DB 241 DSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWKQKQREFKRSIRKLCQ 295

RESULT 2  
 Q96HF1 PRELIMINARY; PRT; 295 AA.  
 AC Q96HF1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Secreted frizzled-related protein 2 (SFRP-2).  
 GN Name=SFRP2; ORFName=UNQ361;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; BC008666; AA08666.1; -  
 DR EMBL; AV359001; AA089360.1; -  
 DR HSSP; 061091; 1IJY.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR000024; Fz domain.  
 DR InterPro; IPR001134; Netrin C.  
 DR InterPro; IPR008993; Timp-like.

DR Pfam; PF01392; Fz; 1.  
 DR Pfam; PF01759; NTR; 1.  
 DR PROSITE; PS50038; Fz; 1.  
 DR PROSITE; PS50189; NTR; 1.  
 SQ SEQUENCE 295 AA; 33518 MW; 97597CFA541BF3D4 CRC64;

Query Match 99.7%; Score 1590; DB 2; Length 295;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-117;  
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQPGSLLLFLASHCCIGSARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60  
 DB 1 MLQPGSLLLFLASHCCIGSARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60  
 QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIOPCHSLCVQ 120  
 DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIOPCHSLCVQ 120  
 QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLHPATEAPKVCACKKNND 180  
 DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLHPATEAPKVCACKKNND 180  
 QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVLWLK 240  
 DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVLWLK 240  
 QY 241 DSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWKQKQREFKRSIRKLCQ 295  
 DB 241 DSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWKQKQREFKRSIRKLCQ 295

RESULT 3  
 O08862 PRELIMINARY; PRT; 295 AA.  
 AC O08862;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Secreted frizzled related protein SFRP-2 (Secreted frizzled-related  
 sequence protein 2).  
 GN Name=Sfrp2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97250455; PubMed=9096311; DOI=10.1073/pnas.94.7.2859;  
 RA Ratner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G.,  
 RA Jenkins N.A., Nathans J.;  
 RT "A family of secreted proteins contains homology to the cysteine-rich  
 ligand-binding domain of frizzled receptors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; BC008666; AA08666.1; -  
 DR EMBL; AV359001; AA089360.1; -  
 DR HSSP; 061091; 1IJY.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR000024; Fz domain.  
 DR InterPro; IPR001134; Netrin C.  
 DR InterPro; IPR008993; Timp-like.





DR PROSITE; PS50038; FZ; 1.  
DR PROSITE; PS50189; NTR; 1.  
SQ SEQUENCE 295 AA; 33501 MW; 2638770C77874C72 CRC64;  
  
Query Match 97.7%; Score 1557; DB 2; Length 295;  
Best Local Similarity 97.6%; Pred. No. 4.8e-115;  
Matches 288; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MLQPGSLLLVLAASHCCCLGSARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRL 60  
DB 1 MPRGPASLLVLAASHCCCLGSARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRL 60  
  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120  
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120  
  
QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNND 180  
DB 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNND 180  
  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
  
QY 241 DSLOQTCCEMNDINAPYLVMGQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 295  
DB 241 DSLOQTCCEMNDINAPYLVMGQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 295  
  
RESULT 6  
ID Q863H1 PRELIMINARY; PRT; 294 AA.  
AC Q863H1; (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DE Putative secreted frizzled related protein 2.  
GN Name=sfrp2;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]\_TaxID=9615;  
RP SEQUENCE FROM N.A.  
RC STRAIN=bred:Irish setter; TISSUE=Retina;  
RA Lin C.T., Cocks J., Pierce-Kelling S., Squire M.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=bred:Irish setter; TISSUE=Retina;  
RA Sargan D.R.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ560716; CAD90762.1; -.  
DR HSSP; O61091; 1IJY.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR000024; Fz\_domain.  
DR InterPro; IPR001134; Netrin C.  
DR Pfam; PF01392; Fz; 1.  
DR Pfam; PF01759; NTR; 1.  
DR SMART; SM00643; C345C; 1.  
DR PROSITE; PS50038; FZ; 1.  
DR PROSITE; PS50189; NTR; 1.  
SQ SEQUENCE 294 AA; 33340 MW; 79C1FF3882CBE1B1 CRC64;  
  
Query Match 97.3%; Score 1550.5; DB 2; Length 294;  
Best Local Similarity 98.0%; Pred. No. 1.6e-114;  
Matches 289; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 MLQPGSLLLVLAASHCCCLGSARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRL 60

Db 1 MPRGPGSLLLVLAASHCCCLGSARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRL 59  
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120  
Db 60 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 119  
QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNND 180  
Db 120 VKDRCAPVMSAFGFPWPMLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNNE 179  
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240  
Db 180 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 239  
QY 241 DSLOQTCCEMNDINAPYLVMGQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 295  
Db 240 DSLOQTCCEMNDINAPYLVMGQKQGGELVITSVKRWQKQREFKRISRSIRKLQ 294  
  
RESULT 7  
ID Q9BG86 PRELIMINARY; PRT; 283 AA.  
AC Q9BG86;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Secreted frizzled-related protein 2 (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RA Levin J.M., Boubaker El Andalousi R.A., Dainat J., Cabrolie M.,  
RA Bacou F.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF323272; AAK11319.1; -.  
DR HSSP; O61091; 1IJY.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR000024; Fz\_domain.  
DR InterPro; IPR001134; Netrin C.  
DR InterPro; IPR008993; TIMP\_like.  
DR Pfam; PF01392; Fz; 1.  
DR Pfam; PF01759; NTR; 1.  
DR SMART; SM00643; C345C; 1.  
DR SMART; SM00063; FRI; 1.  
DR PROSITE; PS50038; FZ; 1.  
DR PROSITE; PS50189; NTR; 1.  
FT NON TER 1  
SQ SEQUENCE 283 AA; 32167 MW; CC75AD7F54DD3ACB CRC64;  
  
Query Match 95.0%; Score 1515; DB 2; Length 283;  
Best Local Similarity 98.6%; Pred. No. 9.6e-112;  
Matches 279; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 13 LASHCCCLGSARGFLFGQPDPSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEV 72  
Db 1 LASHCCCLGSARGFLFGQPDPSYKRSNCKPIPATLQCHGIEYQNRLPNLLGHETMKEV 60  
  
QY 73 LEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVQKRCAPVMSAF 132  
Db 61 LEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVQKRCAPVMSAF 120  
  
QY 133 GFPPMDLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNDDNDIMETLCKN 192  
Db 121 GFPPMDLECDRFPQNDLDCIPLASSDHLHPATEAPKVCEACKNDDNDIMETLCKN 180  
  
QY 193 DFALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLKDSLCQTCCEMND 252





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Db 61 PNLGHETMKEVLEQAGAWIPLVMKQCHPDTKFKLCSLFAFVCLDLDDETIQCHSRVQ 120
Qy 121 VKDRCAPVNSAFGPPMDLECDRPPQNDLCLPIPLASSDHLHPATEEAPKVCACKNKD 180
Db 121 VKDRCAPVNSA--FPPMDLECDRPPQNDLCLPIPLASSDHLHPATEEAPKVCACKNKD 178
Qy 181 DNDIMETLCKNDFALKIKVKEITYNR 208
Db 179 DNDIMETLCKNDFALKIKVKEITYNR 206

RESULT 12
Q6YNR8 PRELIMINARY; PRT; 310 AA.
AC Q6YNR8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
GN Name=frp1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin J., Kim S.H., Yeo S.Y., Huh T.L.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050560; AAL11439.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS50038; FRI; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 310 AA; 35393 MW; 77D3412C6CCC8EA4 CRC64;

Query Match 41.9%; Score 667.5; DB 2; Length 310;
Best Local Similarity 47.2%; Pred. No. 1.1e-44;
Matches 125; Conservative 51; Mismatches 80; Indels 9; Gaps 5;

Qy 33 FSYKRSNCKPIPANLQCHGIEYQNNRLPNLGHETMKEVLEQAGAWIPLVMKQCHPDTK 92
Db 45 FYAKQPCQVDIPADLRLCYNVGVKMWRLPNLGHETMKEVLEQAGAWIPLVMKQCHPDTK 104
Qy 93 KFLCSLFAFVCLDLDDETIQCHSLCVQVKRCAPVNSAFGPPMDLECDRPPQNDLCL 152
Db 105 VFLCSLFAFVC---LDRPIYPCRSLEAVRDSAPVMETYGPPWPEMLQCEKFPIDNLC 161
Qy 153 IPLA--SSDHLHPATE--EAPKVCACKNKDNDNDIMETLCKNDFALKIKVKEITYNR 210
Db 162 IPMQFSAGH---ATQTPVSKVPCPDNELKADT--IMEHYCASDFALKMKIKAKEKGD 217
Qy 211 KIILETKSTIYKLVNGVSRDLKSVLWKLKSLQCTCEBMDINAPYLVMGKQGGELVI 270
Db 218 KLIAQKKVVLKGLKRLKDLKLLTYKNGANCPCSLDNLGNSFLMGRKVDQQLL 277
Qy 271 TSVKRWQKQRFKRSIRKLQC 295
Db 278 MSIHKWDKSKELKPAIKYRSQC 302

RESULT 13
Q8K269 PRELIMINARY; PRT; 314 AA.
ID Q8K269
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AC Q8K269;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted frizzled-related sequence protein 5.
GN Name=Strps;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaltz D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032921; ANH32921.1; -.
DR HSSP; Q61091; IJY.
DR MGD; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS50063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 314 AA; 35409 MW; 29775FF26513B7DA CRC64;

Query Match 39.6%; Score 631; DB 2; Length 314;
Best Local Similarity 44.2%; Pred. No. 9e-42;
Matches 125; Conservative 49; Mismatches 83; Indels 26; Gaps 7;

Qy 19 LGSARGLFLFGQPDFSY-----KRSNCKPIPANLQCHGIEYQNNRLPNLL 64
Db 16 LGALHGAPTRGQ--EYDYGWQAEPHGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLL 74
Qy 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKFKLCSLFAFVCLDLDDETIQCHSLCVQVKDR 124
Db 75 EHESLAIVKQQAASWPLAKRCHSDTQVFLCSLFAFVC---LDRPIYPCRSLEAVRAG 131
Qy 125 CAPVNSAFGPPWPMLECDRPPQNDLCLPIPLASSDHLHPATEEAP---KVCACKNKD 181
Db 132 CAPLMEAYGFPWPEMLCHKEFPDNDLCLPIPLASSDHLHPATEEAP---LDRPIYPCRSLEAVRAG 187
Qy 182 DNDIMETLCKNDFALKIKVKEITYNRDKIILETKSTIYKLVNGVSRDLKSVLWKLK 241
Db 188 DG-LMEQWCSSDFVVKMKRIKEIKIDNGDRKLIQAQKKKLLKAGPLKRDTKKLVLMKN 246
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QY 242 SLQCTCEEMNDINAPYLWGKQGGELVITSVKRWKQKQREFK 284  
Db 247 GASCPQPDNLNLTGSLVNGRKVEGQLLTAVYRWKKNKEMK 289

## RESULT 14

```
Q6GZK1 PRELIMINARY; PRT; 306 AA.
AC Q6GZK1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15210177; DOI=10.1016/j.mod.2004.03.003;
RA Esteve P., Lopez-Rios(1) J., Bovolenta P.;
RT "SFRP1 is required for the proper establishment of the eye field in
RT the medaka fish.";
RL Mech. Dev. 121:687-701 (2004).
DR EMBL; AY560904; AAS59408.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS0038; Fz; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 306 AA; 34955 MW; 6D49B0FB9682C48C CRC64;

Query Match 39.3%; Score 627; DB 2; Length 306;
Best Local Similarity 39.9%; Pred. No. 1.8e-41;
Matches 123; Conservative 54; Mismatches 87; Indels 44; Gaps 9;

QY 9 LLLFLASHCCLGSLGFLFGQPDFSY-----KRSNCKPIPANLQLCHGIE 54
Db 14 LVLLAVTC-----GASEYETWAGSYNGRGYKAPQCVDPDDLRLCHTVG 62

QY 55 YQNMRLPNLLGHETWKEVLEQAGAWIPLVMKQCHPDTKKFICSLFAPVCLDDLDLDTIQPC 114
Db 63 YQMLLPNLLHETWAEVKQQAASSWVPLVHKHCHKDTQVFLCALFAPVC---MERPIYPC 119

QY 115 HSLCVQVKDRCAPVSAFGFPWPMLECDRFPQDNDLCIPLASSDHLLPATEEA-----P 169
Db 120 RWLCTVDSGSPFMEAFGFPPEMLTCDKFPQDG-VCIATVQPN-----ATEATWPSGHS 174

QY 170 KVCEACKN--KNDDNDIMETLCKNDFAKIKVKEITYINRDTKIILETKSKTIYKLVNGV 227
Db 175 PACPPCDNEIKND---AMLENICASEFALKAKIKVQENMDRKVILQ-RRKRMVYKQGNL 230

QY 228 SRDLKKSVLWIKDSLOQTCCEEMNDINAPYLWGKQGGELVITSVKRWKQKQREFK 287
Db 231 KKRDLLKLTLYLKGANCPCQQLLENQYLIMGRKVDKQFLITGIHKWDKSKSEFKKIM 290

QY 288 RSIRKLQ 295
Db 291 KKLKNYKC 298
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RESULT 15  
Q9WU66

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Q9WU66 PRELIMINARY; PRT; 314 AA.
AC Q9WU66;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=Sfrp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR EMBL; AF117759; AAD25053.1; -.
DR HSP; Q61091; IJY.
DR MGB; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS0038; Fz; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 314 AA; 35381 MW; 296847F56D1CAFDD CRC64;

Query Match 39.3%; Score 627; DB 2; Length 314;
Best Local Similarity 43.8%; Pred. No. 1.9e-41;
Matches 124; Conservative 49; Mismatches 84; Indels 26; Gaps 7;

QY 19 LGSARGLFLGQPDFSY-----KRSNCKPIPANLQLCHGIEYQNMRLPNLL 64
Db 16 LGALHGAPTRGQ-EYDYGWQAEPLHGRSYSKPPQCLDIPADLPFLCHTVGYKRMRLPNLL 74

QY 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKKFICSLFAPVCLDDLDLDTIQPCSHSLCVQVKDR 124
Db 75 EHESLAEVKQAASSWLPPLAKRCHSDTQVFLCSLFAPVC---LDRPIYPCSLCEAARAG 131

QY 125 CAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLLPATEAP---KVCEACKNND 181
Db 132 CAPLMEAYGFPWPEMLHCHKPFLDNDLCIAVQFGH--LPAT--APPVTKICAQCEMEHSA 187

QY 182 DNDIMETLCKNDFAKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWIKD 241
Db 188 DG-LMEQWCSDFVYVKRIKEIKIDNGDRKLIGAKKKLLKAGPLKKRDKTKLVLHMKN 246

QY 242 SLQCTCEEMNDINAPYLWGKQGGELVITSVKRWKQKQREFK 284
Db 247 GASCPQPDNLNLTGSLVNGRKVEGQLLTAVYRWKKNKEMK 289
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Search completed: September 1, 2005, 10:54:24  
Job time : 122.518 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2005, 09:26:23 ; Search time 315.5 Seconds  
(without alignments)  
6579.934 Million cell updates/sec

Title: US-08-949-904A-1  
Perfect score: 3585  
Sequence: 1 GAATTCGGCCTTCATGGCCT.....AAAAAAGCGCGCGC 2027

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2\_1/USFTO\_spool\_P/US08949904/runat\_01092005\_102612\_21247/app\_query.fasta\_1.2183  
-DB=UniProt -QFMT=fascan -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08949904 @CEN 1.1 401 @runat\_01092005\_102612\_21247 -NGBU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	44.5	295	Q9HAP5	Q9hap5 homo sapien
2	1590	44.4	295	Q96HF1	Q96hf1 homo sapien
3	1560	43.5	295	O08862	O08862 mus musculus
4	1557	43.4	295	O35297	O35297 mus musculus
5	1557	43.4	295	P97299	P97299 mus musculus
6	1550.5	43.2	294	O863H1	O863h1 canis famil
7	1515	42.3	283	O29B86	O29b86 oryctolagus
8	1318	36.8	295	O6F8B6	O6f8b8 xenopus tro
9	1299	36.2	292	O71A96	O71a96 gallus gall
10	1283	35.8	298	O72XM6	O72xm6 xenopus lae
11	1116	31.1	206	O14778	O14778 homo sapien
12	670.5	18.7	310	O6VNR8	O6vnr8 brachydanio
13	641	17.9	314	O8X269	O8x269 mus musculus
14	637	17.8	314	O9WU66	O9wu66 mus musculus
15	629	17.5	315	O9XSC1	O9xsc1 bos taurus
16	627	17.5	306	O6GZK1	O6gzk1 oryzias lat

17	624	17.4	317	2	O14780	homo sapien
18	618.5	17.3	296	2	Q7C2K9	brachydanio
19	618.5	17.3	315	2	O640J3	xenopus lae
20	613.5	17.1	315	2	Q8AWG4	xenopus lae
21	611.5	17.1	315	2	Q6GL50	xenopus tro
22	608	17.0	313	2	O00546	homo sapien
23	606.5	16.9	314	2	O14779	homo sapien
24	606.5	16.9	314	2	Q8N474	homo sapien
25	603.5	16.8	308	2	O19116	bos taurus
26	597	16.7	314	2	Q8RLJ4	mus musculus
27	595	16.6	314	2	O08861	mus musculus
28	591.5	16.5	272	2	Q8C4U3	mus musculus
29	583.5	16.3	311	2	Q9Y124	xenopus lae
30	575.5	16.1	314	2	Q9DEQ4	gallus gall
31	503.5	14.0	307	2	O42397	gallus gall
32	498	13.9	295	2	Q91897	xenopus lae
33	484.5	13.5	300	2	Q8F2E8	xenopus tro
34	483	13.5	282	2	Q8JHC7	brachydanio
35	468	13.1	121	2	Q919F4	xenopus lae
36	433.5	12.1	280	2	Q91AUS	xenopus lae
37	431.5	12.0	284	2	Q90ZA6	ambystoma m
38	422.5	11.8	281	2	Q73821	xenopus lae
39	413.5	11.5	282	2	Q7SX78	brachydanio
40	399	11.1	77	2	Q80W55	rattus norv
41	380.5	10.6	260	2	Q9GUF5	caenorhabdi
42	351.5	9.8	115	2	Q90ZG8	brachydanio
43	319	8.9	750	2	O810L8	mus musculus
44	314	8.8	158	2	Q9R168	rattus norv
45	303.5	8.5	642	2	Q7TS82	mus musculus

## ALIGNMENTS

### RESULT 1

Q9HAP5 PRELIMINARY; PRT; 295 AA.  
ID Q9HAP5;  
AC Q9HAP5;  
DT 01-MAR-2001 (Tremblérel. 16, Created)  
DT 01-MAR-2001 (Tremblérel. 16, Last sequence update)  
DT 01-MAR-2004 (Tremblérel. 26, Last annotation update)  
DE Pancreas tumor-related protein.  
GN Name=FKSG12;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang Y.-G.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF311912; XAG24923.1  
DR PIR; J0174; J0174.  
DR HSP; G61091; IJY.  
DR Genew; HGNC:10777; SFRP2.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR000024; Fz\_domain.  
DR InterPro; IPR001134; Netrin\_C.  
DR Pfam; PF01392; Fz; 1.  
DR Pfam; PF01759; NTR; 1.  
DR SMART; SM00643; C345C; 1.  
DR SMART; SM00063; FRI; 1.  
DR PROSITE; PS50038; FZ; 1.  
DR PROSITE; PS50189; NTR; 1.  
SQ SEQUENCE 295 AA; 33490 MW; 97597971541BFBC4 CRC64;  
Alignment Scores: 2.16e-90 Length: 295  
Pred. No.: 1594.00 Matches: 295  
Score: 100.00%  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0







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QY 376 AAGCCCATCCGGCCCACTGAGCTGTGCGGCGCATCGAATACCAGAACATGGCGTG 435
Db 41 LysProileProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrGlnAsnMetArgLeu 60
QY 436 CCCAACCTGCTGGCCGACAGACCATGAAGGAGGTGCTGGAGCAGCGCGCTGGATC 495
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
QY 496 CCGCTGTGTCATGAAGCAGTGCACCCGGACACCAAGAACTTCTGTGCTGCTTTCGCC 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCGCTGTGCTGATGACCTAGACAGACCATCCAGCCATCGCTGCTGCTGCGTGAG 615
Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAGGACCGTGGCCCGGCTCATGTCGCGCTTCCGCTTCCCTGGCCGACATGCTT 675
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
QY 676 GAGTGGACCGTTTCCCGGACGACACGACCTTTCGATCCCTCGCTAGCAGCACAC 735
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATGTGAAGCTTCCGAGCTGCAAAATGAT 795
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysThrLysAsnGlu 180
QY 796 GATGACAAACGACATATGTAAGACGCTTTGTAATAATGATTTTGGCACTGAAATAAAGTG 855
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGCAAGACC 915
Db 201 LysGluIleThrTyriLeAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
QY 916 ATTACAAAGCTGAACGGTGTGTCGAAAGGACCTGGAAGAAATCGTGCTGGCTCAA 975
Db 221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValIleTrpLeuLys 240
QY 976 GACAGCTTCAGTGCACCTGTGAGAGATGAACAGCATCAACCGCCCTTATCTGCTCATG 1035
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260
QY 1036 GGACAGAAACAGGGTGGGAGCTGTGATACCTCGGTGAACGGTGGAGAGAGCGGAG 1095
Db 261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295

RESULT 4
O35297 PRELIMINARY; PRT; 295 AA.
AC O35297;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted apoptosis related protein 1.
CN Name=Sfrp2; Synonyms=Sarp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
RA Melkonyan H.S., Chang W.C., Shapiro J.P., Mahadevappa M.,
RA Fitzpatrick P.A., Kiefer M.C., Tomei L.D., Umansky S.R.;
RT "SARPs: a family of secreted apoptosis-related proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).
```

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[2]
RP SEQUENCE FROM N.A.
RA Melkonyan H., Prochazka V., Umansky S.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF01989; AAB70795.1; -.
DR HSP; O61091; I1UJ.
DR MGD; MGI:108078; Sfrp2.
DR GO; GO:0005635; C:extracellular space; TAS.
DR InterPro; IPR000024; F2 domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS00038; FZ; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 295 AA; 33483 MW; 2D296C477C958762 CRC64;

Alignment Scores:
Pred. No.: 4.21e-88 Length: 295
Score: 1557.00 Matches: 288
Percent Similarity: 98.64% Conservative: 3
Best Local Similarity: 97.63% Mismatches: 4
Query Match: 43.43% Indels: 0
Db: 2 Gaps: 0

US-08-949-904A-1 (1-2027) x O35297 (1-295)
QY 256 ATGTCGACGGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
Db 1 MetProArgGlyProAlaSerLeuLeuLeuValLeuAlaSerHisCysCysLeuGly 20
QY 316 TCGCGCGCGCGGCTTCTCTCTTTGGCCAGCCCGACTTCTCTACAAAGCGCAATTCG 375
Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgThrAsnCys 40
QY 376 AAGCCCATCCCGGCAACCTGCGCTGTCGACCGCATCGAATACCAGAACATCGGCGTG 435
Db 41 LysProileProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrGlnAsnMetArgLeu 60
QY 436 CCCAACCTGCTGGCCGACAGACCATGAAGGAGGTGCTGGAGCAGCGCGCTGGATC 495
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
QY 496 CCGCTGTGTCATGAAGCAGTGCACCCGGACACCAAGAACTTCTGTGCTGCTTTCGCC 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCGCTGTGCTGATGACCTAGACAGACCATCCAGCCATCGCTGCTGCTGCGTGAG 615
Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAGGACCGCTGCGCCCGGCTCATGTCGCGCTTCCGCTTCCCTGGCCGACATGCTT 675
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
QY 676 GAGTGGACCGTTTCCCGGACGACACGACCTTTCGATCCCTCGCTAGCAGCACAC 735
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATGTGAAGCTTCCGAGCTGCAAAATGAT 795
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysThrLysAsnGlu 180
QY 796 GATGACAAACGACATATGTAAGACGCTTTGTAATAATGATTTTGGCACTGAAATAAAGTG 855
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGCAAGACC 915
Db 201 LysGluIleThrTyriLeAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
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QY 1002 GATGAACGACATCAACGCCCTTATCTGGTCTATGGGACAGAAACAGGGTGGGAGCTGGT 1061
Db 254 nleuaspAnLeuThrGlySerPheLeuValMetGlyArgLysValGluGlyGlnLeuLe 274
QY 1062 GATCACCTCGGTGAACGGCTGGCAGAAAGGGCGGACAGAGAGTTCAAG 1107
Db 274 uleuthrAlaValTyArgTrpAspLysLysAnLysGluMetLys 289

RESULT 14
Q9WU66
ID Q9WU66 PRELIMINARY; PRT; 314 AA.
AC Q9WU66;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=Sfrp5;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR EMBL; AF117759; AAD25053.1; -.
DR HSSP; Q61091; 11JY.
DR MGD; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 314 AA; 35381 MW; 296847P56D1CAPDD CRC64;

Alignment Scores:
Pred. No.: 3.58e-31 Length: 314
Score: 637.00 Matches: 132
Percent Similarity: 58.23% Conservative: 52
Best Local Similarity: 41.77% Mismatches: 91
Query Match: 17.77% Indels: 41
DB: 2 Gaps: 7

US-08-949-904A-1 (1-2027) x Q9WU66 (1-314)
QY 186 GCTGAACCTCGCGCGCTCGCCCTTCCCGGCTCGCTCCCTCGCTCCGCTCGGCTCG 245
Db 7 AlaArgThrAlaAlaLeuAlaLeuLeuGlyAlaLeuHisGlyAlaProThrArgGly 26
QY 246 CGCGCCCGACGATGCTGCAGGGGCCCTGGCTCGTGTGCTCTCTTCCTCGCCTCGCACTG 305
Db 27 GlnGluTyArgTy-Tyr-Gly----- 33
QY 306 CTGCTGGCTCGCGCGCGGCTCTTCTCTTGGCCAGCCGCTCTCTCTCAACAGG 365
Db 34 -----TTPGlnAlaGluProLeu-HisGlyAr 42
QY 366 CAGCAATTGCAAGCCC-----ATCCCGGCCAACCTGCAGCTGTGCCACGG 410
Db 42 gSerTySerLysProProGlnCysLeuAspLeuProAlaAspLeuProLeuCysHisTh 62
QY 411 CATCAATACCAAGACATCGCGCTGCCCACTGCTGGGCCACGACGACCATGAAGAGGT 470
Db rValGlyTyLysArgMetArgLeuProAnLeuGluHisGluSerLeuAlaGluVa 82

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QY 471 GCTGGAGCAGCGCCGGCGCTTCGATCCCGCTCGTTCATGAAGCAGTGCACCGGACACCAA 530
Db 82 llyeGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCysHisSerAspThrGl 102
QY 531 GAAGTTCTGCTGCTGCTTCCTCGCCCGCTGCTGCTCGATGACCTAGACGAGACCATCCA 590
Db 102 nValPheLeuCysSerLeuPheAlaProValCys-----LeuAspArgProIleTy 119
QY 591 GCCATGCCACTCGCTCTGCTGTCAGGTGAAGACCGCTGCGCCCGCTCATGTCCGCTT 650
Db 119 rProCysArgSerLeuCysGluAlaAlaArgAlaGlyCysAlaProLeuMetGluAlaTy 139
QY 651 CGGCTTCCCTGCGCCGACATGCTTGAGTGCAGCGCTTCCCGGACGACGACCTTTG 710
Db 139 rGlyPheProTrpProGluMetLeuHisCysHisLysPheProLeuAspAsnLeuCy 159
QY 711 CATCCCTCGCTAGCAGCACCCTCTCTCCAGCCACCGGAGGAGCTCCA----- 762
Db 159 sileAlaValGlnPheGlyHis-----LeuProAlaThr-----AlaProProValTh 175
QY 763 -AAGGTATGTGAAGCCTGCAAAAATAAATAATGATGATGACAAACGACATAATGGAAACGCT 821
Db 175 rLysileCysAlaGlnCysGluMetGluHisSerAlaAspGly--LeuMetGluGlnMe 194
QY 822 TTGTAATAATGATTTGCACTGAAATAAAGTGAAGGAGATAACCTACATCAACCGAGA 881
Db 194 tCysSerSerAspPheValValLysMetArgileGlyLeuLysileAspAsnGlyAs 214
QY 882 TACCAAAATCATCTGGAGACCAAGAGCAACACCATTTACAAGCTGAACGGTGTGTCCGA 941
Db 214 pArgLysleuileGlyAlaGlnLysLysLysLeuLysAlaGlyProLeuLysAr 234
QY 942 AAGGACCTGAAGAAATCGTGTGCTGCTCAAAAGACAGCTTGCAGTGCACCTGTGAGA 1001
Db 234 gLysAspThrLysLysLeuValLeuHisMetLysAsnGlyAlaSerCysProCysProGl 254
QY 1002 GATGAACGACATCAACGCCCTTATCTGGTCTATGGGACAGAAACAGGGTGGGAGCTGGT 1061
Db 254 nLeuAspAnLeuThrGlySerPheLeuValMetGlyArgLysValGluGlyGlnLeuLe 274
QY 1062 GATCACCTCGGTGAACGGCTGGCAGAAAGGGCGGACAGAGAGTTCAAG 1107
Db 274 uleuthrAlaValTyArgTrpAspLysLysAnLysGluMetLys 289

RESULT 15
Q9XSC1
ID Q9XSC1 PRELIMINARY; PRT; 315 AA.
AC Q9XSC1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=sfrp5;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR EMBL; AF117757; AAD25051.1; -.
DR HSSP; Q61091; 11JY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.

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DR InterPro: IPR008993; TIMP\_like.  
DR Pfam: PF01392; Fz; 1.  
DR Pfam: PF01759; NTR; 1.  
DR SMART: SM00643; C345C; 1.  
DR SMART: SM00063; FRI; 1.  
DR PROSITE: PS0038; FZ; 1.  
DR PROSITE: PS0189; NTR; 1.  
SQ SEQUENCE 315 AA; 35279 MW; 8B6E94951060A976 CRC64;

Alignment Scores:  
Pred. No.: 1,12e-30 Length: 315  
Score: 629.00 Matches: 132  
Percent Similarity: 57.14% Conservative: 52  
Best Local Similarity: 40.99% Mismatches: 97  
Query Match: 17.55% Indels: 41  
DB: 2 Gaps: 7

US-08-949-904A-1 (1-2027) x Q9XSC1 (1-315)

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QY 168 AGAGCGGCGCCGACAACTCGAAGTCCGGCGCGCTCGCCCTCCCGGCTCCGCTCCC 227
Db 2 ArgAlaAlaAlaGlyGlyAlaArgAlaAlaValLeuAlaLeuLeuGlyAlaLeuHis 21
QY 228 TCTGCCCCCTCGGGTCGGCGCCACAGATGTCGACGGCCCTGGCTCGCTGCTGCT 287
Db 22 GlyAlaProAlaArgGlyGluGluTyrAspTyrTyrGly----- 34
QY 288 CTTCTCTCGCTCGCACTGCTGCTGGCTCGGCGCGGGCTCTTCTCTTTGGCCAGCC 347
Db 35 -----trp-GlnTh 37
QY 348 CGACTTCTCTACAGCGCAGCAATTCAGGCC-----ATCCCGGCCAA 392
Db 37 rGluProLeuHisGlyArgSerTyrSerLysProGlnCysLeuAspIleProAlaAs 57
QY 393 CTGCACTGTGCGCAGGATCGAATACCAAGACATCGCGCTGCCAACCTGCTGGGCCA 452
Db 57 pleuProLeuCysHisThrValGlyTyrLysArgMetArgLeuProAsnLeuLeuGluHi 77
QY 453 CGAGACCATGAAGAGTCTCGAGCAGCGCGCTTGGATCCGCTGCTCATGAAGCA 512
Db 77 sGluSerLeuAlaGluValLysGlnGlnAlaSerSerTyrLeuProLeuLeuAlaLysAr 97
QY 513 GTGCCACCCGACACCAAGATTCCTGTCTCGCTCTTCCGCCCGCTGCTGCTCGATGA 572
Db 97 gCysHisSerAspThrGlnValPheLeuLeuCysSerLeuPheAlaProValCys----- 114
QY 573 CCTAGACGAGACCATCCAGCATGCCACTCGCTCTGCTGCGTAGGTAAGGACCGCTGCC 632
Db 115 -LeuAspArgProIleTyrProCysArgSerLeuCysGluAlaValArgAlaGlyCysAl 134
QY 633 CCGGTCATGTCGGCTTCCTCCCTGCGCCGACATGCTTGAGTGGACCGTTTCCC 692
Db 134 aProLeuMetGluAlaTyrGlyPheProTyrProGluMetLeuHisCysHisLysPhePr 154
QY 693 CCAGGACAAACGCTTTGATCCCTCGCTCGTAGCAGCAGCACCTCTCCAGCCACCGA 752
Db 154 oLeuAspAsnAspLeuCysIleAlaValGlnPheGlyHis-----LeuProAlaThr-- 171
QY 753 GGAAGCTCCA-----AAGGTATGTGAAGCTTGCAAAAATAAAATGATGATGACAA 803
Db 172 ----AlaProProValThrLysIleCysAlaGlnCysGluMetGluHisSerAlaAspGl 190
QY 804 CGACATAATGGAACCGCTTTGATAAAATGATTTTGCACCTGAAATAAAGTGAAGGAGAT 863
Db 190 y--LeuMetGluGlnMetCysSerSerAspPheValValLysMetArgIleLysGluIl 209
QY 864 AACCTACATCAACCGAGATACCAAAATCATCTGAGACCAAGACAGACCATTTACAA 923
Db 209 eLysIleGluAenGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLeuLeuLy 229
QY 924 GCTGAACGGTGTGTCGGAAGGAGCCTGAAGAAATCGGTGTGCTCGCTCAAGACAGCTT 983
Db 924 -----
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Db 229 sSerGlyProLeuLysArgLysAspThrLysArgLeuValLeuHisMetLysAsnSerAl 249
QY 984 GCAGTGCACCTGTGAGGAGATGAACGACATCAACGCCGCCCTATCTGGTCAATGGACAGAA 1043
Db 249 aGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArgLy 269
QY 1044 ACAGGTCGGGAGCTGGTGATCACCTCGTGAAGCGGTGGCAGAAAGGGGCGACAGAGATT 1103
Db 269 eValAspGlyGlnLeuLeuMetAlaValTyrArgTrpAspLysLysAsnLysGluMe 289
QY 1104 CAAG 1107
Db 289 tLys 290
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Search completed: September 1, 2005, 09:37:15  
Job time : 327.5 secs

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